GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:          December 13, 2003, 04:37:24 ; Search time 1755.93 Seconds
                                             (without alignments)
                                             7460.491 Million cell updates/sec


Title:           US-09-852-261-3
Perfect score:   539
Sequence:        1 ggaccagagaccctttgcgg..........agtaaacattcccggaattc 539


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


Searched:        22781392 seqs, 12152238056 residues


Total number of hits satisfying chosen parameters:       45562784


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
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                 6:   em_estpl:*
                 7:   em_estro:*
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                 11:  gb_htc:*
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                 21:  em_gss_fun:*
                 22:  em_gss_mam:*
                 23:  em_gss_mus:*
                 24:  em_gss_pro:*
                 25:  em_gss_rod:*
                 26:  em_gss_phg:*
                 27:  em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| c | 1 | 501.6 | 93.1 | 549 | 9 | AI169253 | AI169253 EST215088 |
| | 2 | 480.4 | 89.1 | 614 | 14 | CD373004 | CD373004 UI-R-GR0- |
| c | 3 | 469.2 | 87.1 | 558 | 9 | AI503976 | AI503976 vm43d08.x |
| c | 4 | 453.4 | 84.1 | 623 | 9 | AW146128 | AW146128 um37e10.x |
| c | 5 | 450.4 | 83.6 | 468 | 9 | AI169770 | AI169770 EST215669 |
| c | 6 | 446.8 | 82.9 | 558 | 9 | AI265629 | AI265629 uj04b07.x |
| c | 7 | 437 | 81.1 | 653 | 13 | BQ200567 | BQ200567 UI-R-DZ1- |
| | 8 | 431.8 | 80.1 | 594 | 10 | BF383724 | BF383724 602044632 |
| | 9 | 425.2 | 78.9 | 816 | 9 | AI119218 | AI119218 ue94h02.y |
| c | 10 | 423 | 78.5 | 499 | 9 | AW495481 | AW495481 UI-M-BH3- |
| c | 11 | 421.2 | 78.1 | 642 | 9 | AI876493 | AI876493 uj59b10.x |
| c | 12 | 402.6 | 74.7 | 525 | 9 | AA963258 | AA963258 UI-R-E1-g |
| c | 13 | 401.6 | 74.5 | 500 | 9 | AA945553 | AA945553 EST201052 |
| c | 14 | 399.4 | 74.1 | 525 | 9 | AI599751 | AI599751 EST251454 |
| c | 15 | 395 | 73.3 | 499 | 12 | BI294072 | BI294072 UI-R-DK0- |
| c | 16 | 394.2 | 73.1 | 502 | 9 | AI104669 | AI104669 EST213958 |
| c | 17 | 367 | 68.1 | 470 | 9 | AI233293 | AI233293 EST229981 |
| c | 18 | 362.6 | 67.3 | 521 | 9 | AW493459 | AW493459 UI-M-BH3- |
| | 19 | 362.6 | 67.3 | 621 | 12 | BI221656 | BI221656 602936980 |
| | 20 | 362.6 | 67.3 | 1658 | 11 | AK081019 | AK081019 Mus muscu |
| | 21 | 361.6 | 67.1 | 559 | 12 | BI715603 | BI715603 ic34h10.y |
| c | 22 | 361.6 | 67.1 | 595 | 9 | AI573421 | AI573421 mo04b11.x |
| | 23 | 361.6 | 67.1 | 602 | 13 | BU590710 | BU590710 AGENCOURT |
| c | 24 | 360 | 66.8 | 499 | 12 | BI676839 | BI676839 ic56a08.x |
| | 25 | 355.2 | 65.9 | 559 | 12 | BI715465 | BI715465 ic33b09.y |
| c | 26 | 352.4 | 65.4 | 477 | 9 | AA800127 | AA800127 EST189624 |
| c | 27 | 350.4 | 65.0 | 561 | 12 | BI714874 | BI714874 ic33b09.x |
| c | 28 | 349.2 | 64.8 | 470 | 9 | AA945027 | AA945027 EST200526 |
| c | 29 | 348 | 64.6 | 564 | 12 | BI714981 | BI714981 ic34h10.x |
| | 30 | 346.4 | 64.3 | 558 | 12 | BI715475 | BI715475 ic33c08.y |
| c | 31 | 341.4 | 63.3 | 464 | 10 | BE104013 | BE104013 UI-R-BX0- |
| c | 32 | 339.4 | 63.0 | 448 | 9 | AW252120 | AW252120 UI-R-BJ0- |
| | 33 | 338 | 62.7 | 882 | 9 | AI604642 | AI604642 vm43d08.y |
| c | 34 | 335.6 | 62.3 | 464 | 12 | BI277678 | BI277678 UI-R-CZ0- |
| c | 35 | 333.6 | 61.9 | 452 | 9 | AW525416 | AW525416 UI-R-BJ0p |
| | 36 | 329.6 | 61.2 | 665 | 9 | AA690767 | AA690767 vu57d12.r |
| | 37 | 329.4 | 61.1 | 799 | 9 | AI314558 | AI314558 uj48d07.y |
| c | 38 | 327.4 | 60.7 | 460 | 9 | AA924219 | AA924219 UI-R-A1-d |
| c | 39 | 326 | 60.5 | 429 | 9 | AI101163 | AI101163 EST210452 |
| | 40 | 323.2 | 60.0 | 773 | 12 | BI144500 | BI144500 602908689 |
| c | 41 | 321.4 | 59.6 | 637 | 9 | AW413016 | AW413016 uq49h08.x |
| | 42 | 316 | 58.6 | 949 | 14 | CB589117 | CB589117 AGENCOURT |
| c | 43 | 311.6 | 57.8 | 445 | 10 | BG071465 | BG071465 H3099C09- |
| | 44 | 310.4 | 57.6 | 473 | 9 | AA451360 | AA451360 vf84g03.r |
| c | 45 | 300.4 | 55.7 | 474 | 9 | AI526955 | AI526955 uj48d07.x |

RESULT 1
AI169253/c
LOCUS        AI169253                    549 bp     mRNA      linear    EST 08-JAN-1999
DEFINITION   EST215088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
             RKIBP33 3' end, mRNA sequence.
ACCESSION    AI169253
VERSION      AI169253.1  GI:4134375
KEYWORDS     EST.
SOURCE       Rattus sp.
  ORGANISM   Rattus sp.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
             Rattus.
REFERENCE    1  (bases 1 to 549)
  AUTHORS    Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
             Kerlavage,A.R. and Adams,M.D.
  TITLE      Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
             Gene Index
  JOURNAL    Unpublished
COMMENT      On Oct 6, 1998 this sequence version replaced gi:3705561.
             Other_ESTs: TC50779
             Contact: Lee, NH
             The Institute for Genomic Research
             9712, Medical Center Drive, Rockville, MD 20850, USA
             Tel: (301)-838-3529
             Fax: (301)-838-0208
             Email: nhlee@tigr.org
             Seq primer: M13-21.
FEATURES             Location/Qualifiers
     source          1. .549
                     /organism="Rattus sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:10118"
                     /clone="RKIBP33"
                     /clone_lib="Normalized rat kidney, Bento Soares"
                     /note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI"
BASE COUNT        112 a     140 c     133 g     164 t
ORIGIN

  Query Match              93.1%;  Score 501.6;  DB 9;  Length 549;
  Best Local Similarity    97.3%;  Pred. No. 3.7e-107;
  Matches  510;  Conservative   0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       8 AGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCAAGGGGCT 67
           |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db     549 AGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAATTCGTGTGTGGACCAAGGGGCT 490

Qy      68 TTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAGACGGGCA 127
           |||||||||||||||||||||| ||||||||||||||||||| ||||||||||||||||||
Db     489 TTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGAAGGGCACCACAGACGGGCA 430

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Qy    128 TTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGTCC 187
          |||||||||||||| |||||||||||||||||||||||||||||||||||||||||| |
Db    429 TTGTGGATGAGTGTAGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCTC 370

Qy    188 GCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACATGCCCA 247
            ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    369 CGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACATTGACATGCCCA 310

Qy    248 AGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGGA 307
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 AGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGGA 250

Qy    308 AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAATG 367
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    249 AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACTTACAGAATG 190

Qy    368 TAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCTGCTTG 427
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 TAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCTGCTTG 130

Qy    428 AGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATATCATTTC 487
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    129 AGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTTC 70

Qy    488 AGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
          ||||||||||||||||||||||||||||||||||||||||||||
Db     69 AGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 26
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RESULT 2
CD373004

```
LOCUS       CD373004                  614 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-R-GR0-csv-j-17-0-UI.r1 UI-R-GR0 Rattus norvegicus cDNA clone
            UI-R-GR0-csv-j-17-0-UI 5', mRNA sequence.
ACCESSION   CD373004
VERSION     CD373004.1  GI:31157094
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 614)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: James Lin, University of Iowa
```

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/rat.html
Seq primer: M13 REVERSE.

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FEATURES                Location/Qualifiers
     source             1. .614
                        /organism="Rattus norvegicus"
                        /mol_type="mRNA"
                        /strain="Sprague-Dawley"
                        /db_xref="taxon:10116"
                        /clone="UI-R-GR0-csv-j-17-0-UI"
                        /tissue_type="Whole embryo"
                        /dev_stage="embryo 13dpc"
                        /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                        /clone_lib="UI-R-GR0"
                        /note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
                        UI-R-GR0 is a cDNA library containing the following
                        tissue(s): rat whole embryo 13dpc. The library was
                        constructed according to Bonaldo, Lennon and Soares,
                        Genome Research, 6:791-806, 1996. Denatured RNA was size
                        fractionated on a 1% agarose gel. First strand cDNA
                        synthesis was primed with oligo-dT primer containing a Not
                        I site. Double strand cDNA was size selected according to
                        mRNA size fraction, ligated with EcoR I adaptor, digested
                        with NotI and then cloned directionally into pYX-Asc
                        vector. The library tag sequence located between the Not I
                        site and the polyA tail is CATCTCTACT. This library was
                        created for the University of Iowa Program for Rat Gene
                        Discovery and Mapping (Val Sheffield, Bento Soares and Tom
                        Casavant)."
BASE COUNT       171 a      168 c      154 g      119 t        2 others
ORIGIN
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  Query Match              89.1%;   Score 480.4;   DB 14;   Length 614;
  Best Local Similarity    97.6%;   Pred. No. 3.5e-102;
  Matches  487;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

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Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      116 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 175

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db      176 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 235

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      236 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 295

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            ||||   |        ||||||||||||||||||||||||||||||||||||||||||||||
Db      296 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 355

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
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```

```
Db     356 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 415

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
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Db     416 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 475

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||||||||
Db     476 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATTCCACGTCACCGCATGATCCTTTG 535

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
           |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db     536 CTGCTTGAGCAACCTGCANAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 595

Qy     481 TCATTTCAGAGATGGGCAT 499
           |||||||||||||||||||
Db     596 CCATTTCAGAGATGGGCAT 614


RESULT 3
AI503976/c
LOCUS       AI503976               558 bp    mRNA    linear   EST 11-MAR-1999
DEFINITION  vm43d08.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA
            clone IMAGE:1001007 3' similar to gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AI503976
VERSION     AI503976.1  GI:4401827
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:565223
            This clone was previously sequenced on the 5' end only, this new
            data is from the 3' end
            High quality sequence stop: 440.
FEATURES             Location/Qualifiers
     source          1..558
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
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                         /clone="IMAGE:1001007"
                         /tissue_type="diaphragm"
                         /dev_stage="adult"
                         /lab_host="SOLR (kanamycin resistant)"
                         /clone_lib="Stratagene mouse diaphragm (#937303)"
                         /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
                         EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA
                         prepared from diaphragm muscle.  Primer: Oligo dT. Average
                         insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor
                         sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
                         CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT        103 a      133 c     149 g      173 t
ORIGIN
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  Query Match                87.1%;  Score 469.2;  DB 9;   Length 558;
  Best Local Similarity      92.8%;  Pred. No. 1.5e-99;
  Matches  492;  Conservative     0;  Mismatches    38;  Indels    0;  Gaps     0;
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Qy         1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
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Db       530 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 471

Qy        61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
             ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |||
Db       470 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 411

Qy       121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
             || |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       410 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 351

Qy       181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
             |||| ||       |||||||||||  |||| || || ||||| |||||||||||||||||
Db       350 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 291

Qy       241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
             |||||||||||||||||||||||| | ||||||||||| ||||||||| |||||||||||
Db       290 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 231

Qy       301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       230 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 171

Qy       361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
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Db       170 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 111

Qy       421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
             ||||||||||||||||||||||||||||| ||||||| ||||||| |||||||| ||| |||||
Db       110 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 51

Qy       481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
             |||| || |||||||||||||||| |||||||||| ||||||||||||||
Db        50 ACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATTC 1
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RESULT 4
AW146128/c

```
LOCUS       AW146128                  623 bp    mRNA     linear   EST 10-OCT-2000
DEFINITION  um37e10.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
            IMAGE:2247498 3' similar to gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AW146128
VERSION     AW146128.1  GI:6167864
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 623)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished
  COMMENT   Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1006958
            Seq primer: custom primer used
            High quality sequence stop: 499.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2247498"
                     /dev_stage="embryo, 14 dpc"
                     /lab_host="DH10B"
                     /clone_lib="Sugano mouse embryo mewa"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer   [ATGTGGCCTTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert.  Size selection was performed to exclude fragments
                     <1.5kb.  Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science).
                     Custom primers  for sequencing: 5' end primer
                     CTTCTGCTCTAAAAGCTGCG and 3' end primer
                     CGACCTGCAGCTCGAGCACA."
BASE COUNT      123 a      138 c      170 g      191 t        1 others
ORIGIN
```

    Query Match              84.1%;  Score 453.4;  DB 9;  Length 623;

Best Local Similarity    92.1%;   Pred. No. 7.5e-96;
Matches  489;  Conservative    0;  Mismatches   41;  Indels    1;  Gaps    1;

```
Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||||||||||||| |||||||||||||||| ||||||||||||||||||||||||||
Db      541 GGACCAGAGACCCTTTTCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 482


Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||| |||
Db      481 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 422


Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || |||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||
Db      421 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAAATGTAC 362


Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            |||| ||      |||||||||| |||| || || ||||| ||||||||||||||||||||
Db      361 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 302


Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            ||||||||||||||||||||||||| | ||||||||||| ||||||||| ||||||||||
Db      301 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 242


Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
            |||||||||||||||| ||||||||| |||||||||||||||||||||||||||||||||
Db      241 AGAAGGAAAGGAAGTACATTTGAAGAACCCAAGTAGAGGAAGTGCAGGAAACAAGACCTA 182


Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            |||||||||||||||||||||||| ||| |||||||||||| ||||||||||| |||||||
Db      181 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 122


Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            |||||||||||||||||||||||||| ||| ||| |||||||| ||||||| ||| |||||
Db      121 CTGCTTGAGCAACCTGCAAAACATCGAAACCCCTACCAAATAACAATAATAAGTCCAATA 62


Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
            ||||| || |||||||||||||||| ||||||||| |||||||||||||||
Db       61 ACATTACAAAGATGGGCATTTCCC-CAATGAAATATACAAGTAAACATTCC 12
```

RESULT 5
AI169770/c

```
  Query Match              83.6%;  Score 450.4;  DB 9;   Length 468;
  Best Local Similarity    97.6%;  Pred. No. 3.6e-95;
  Matches  457;  Conservative    0;  Mismatches  11;  Indels   0;  Gaps    0;


Qy      63 GGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAGAC 122
           ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     468 GGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAGAC 409


Qy     123 GGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTG 182
           |·|||||||||||||||||||||||| |||||||||||||||||||||||| |||||||||||
Db     408 GGGCATTGTGGATGAGTGTTGCTCCCGGAGCTGTGATCTGAGGAGGTTGGAGATGTACTG 349


Qy     183 TGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACAT 242
           || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     348 TGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACAT 289


Qy     243 GCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAG 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     288 GCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAG 229


Qy     303 AAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACA 362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     228 AAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACA 169


Qy     363 GAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCT 422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     168 GAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCT 109


Qy     423 GCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATATC 482
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     108 GCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACC 49


Qy     483 ATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
           ||||||||||||||||||||||||||||||||||||||||||||||||
```

Db          48 ATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 1


RESULT 6
AI265629/c
LOCUS          AI265629                558 bp      mRNA      linear    EST 18-NOV-1998
DEFINITION     uj04b07.x1 Sugano mouse liver mlia Mus musculus cDNA clone
               IMAGE:1890901 3' similar to gb:X04482 Mouse mRNA for
               preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION      AI265629
VERSION        AI265629.1  GI:3883787
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
  ORGANISM     Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1  (bases 1 to 558)
  AUTHORS      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
               Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
               Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
               Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
               Waterston,R.
  TITLE        The WashU-HHMI Mouse EST Project
  JOURNAL      Unpublished
  COMMENT      Contact: Marra M/Mouse EST Project
               WashU-HHMI Mouse EST Project
               Washington University School of MedicineP
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: mouseest@watson.wustl.edu
               This clone is available royalty-free through LLNL ; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               MGI:975225
               Seq primer: custom primer used
               High quality sequence stop: 495.
FEATURES                 Location/Qualifiers
        source           1. .558
                         /organism="Mus musculus"
                         /mol_type="mRNA"
                         /strain="C57BL"
                         /db_xref="taxon:10090"
                         /clone="IMAGE:1890901"
                         /sex="female"
                         /dev_stage="adult"
                         /lab_host="DH10B"
                         /clone_lib="Sugano mouse liver mlia"
                         /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
                         (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                         was primed with an oligo(dT) primer
                         [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                         ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                         and cloned into distinct DraIII sites of the pME18S-FL3
                         vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                         be used to isolate the cDNA insert.  Size selection was
                         performed to exclude fragments <1.5kb.  Library
                         constructed by Dr. Sumio Sugano (University of Tokyo

Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."

BASE COUNT      106 a      135 c      156 g      161 t
ORIGIN

  Query Match              82.9%;   Score 446.8;   DB 9;   Length 558;
  Best Local Similarity    92.7%;   Pred. No. 2.6e-94;
  Matches 469;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      506 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 447

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||| |||
Db      446 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 387

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      386 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 327

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            |||| ||        ||||||||||| |||| || || ||||| |||||||||||||||||
Db      326 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 267

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            ||||||||||||||||||||||||||| | |||||||||||| |||||||| |||||||||||
Db      266 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 207

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      206 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 147

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            ||||||||||||||||||||||| ||| |||||||||||||| |||||||| |||||||||
Db      146 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 87

Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            |||||||||||||||||||||||||||| |||||||| |||||||| |||||||| ||| |||||
Db       86 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 27

Qy      481 TCATTTCAGAGATGGGCATTTCCCTC 506
            |||| || ||||||||||||||||| |
Db       26 ACATTACAAAGATGGGCATTTCCCCC 1


RESULT 7
BQ200567/c
LOCUS       BQ200567                 653 bp    mRNA    linear    EST 02-MAY-2002
DEFINITION  UI-R-DZ1-cne-a-18-0-UI.s1 UI-R-DZ1 Rattus norvegicus cDNA clone
            UI-R-DZ1-cne-a-18-0-UI 3', mRNA sequence.
ACCESSION   BQ200567
VERSION     BQ200567.1  GI:20417032
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus

```
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                  Rattus.
REFERENCE    1  (bases 1 to 653)
  AUTHORS    Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE      Normalization and subtraction: two approaches to facilitate gene
             discovery
  JOURNAL    Genome Res. 6 (9), 791-806 (1996)
  MEDLINE    97044477
   PUBMED    8889548
  COMMENT    Contact: Soares, MB
             Coordinated Laboratory for Computational Genomics
             University of Iowa
             375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
             Tel: 319 335 8250
             Fax: 319 335 9565
             Email: bento-soares@uiowa.edu
             The sequence contained an oligo-dT track that was present in the
             oligonucleotide that was used to prime the synthesis of first
             strand cDNA and therefore this may represent a bonafide poly A
             tail. The sequence tag present in the cDNA between the NotI site
             and the oligo-dT track served to verify it as a clone from the
             normalized cartilaginous tumor library cDNA Library Preparation:
             M.B. Soares Lab Clone distribution: clones will be available
             through Research Genetics (www.resgen.com) The following repetitive
             elements were found in this cDNA sequence: 1-43,
             >AT_rich#Low_complexity 118-164, >POLY_A#Simple_repeat
             Seq primer: M13 Forward
             POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .653
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-DZ1-cne-a-18-0-UI"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="37 days"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-DZ1"
                     /note="Organ: Spine; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     UI-R-DZ1 is a normalized cDNA library containing the
                     following tissue(s): Swarm Rat Chondrosarcoma. The library
                     was constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CATTCTTGTA. The Rat cartilaginous tumor tissue was
                     provided by Dr Jeff Stevens at the University of Iowa.
                     TAG_LIB=UI-R-DZ1
                     TAG_TISSUE=cartilaginous tumor
```

TAG_SEQ=CATTCTTGTA"
BASE COUNT        134 a     137 c     137 g     245 t
ORIGIN

  Query Match              81.1%;   Score 437;   DB 13;   Length 653;
  Best Local Similarity    97.6%;   Pred. No. 5.3e-92;
  Matches   454;   Conservative     0;   Mismatches   10;   Indels   1;   Gaps     1;

Qy       67 TTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAGACGGGC 126
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db      653 TTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAGACGGGC 594

Qy      127 ATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGTC 186
            ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db      593 ATTGTGGATGAGTG-TGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCT 535

Qy      187 CGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACATGCCC 246
            |        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      534 CCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACATGCCC 475

Qy      247 AAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGG 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      474 AAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGG 415

Qy      307 AAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAAT 366
            '   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      414 AAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAAT 355

Qy      367 GTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCTGCTT 426
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db      354 GTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGTTGCTT 295

Qy      427 GAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATATCATTT 486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db      294 GAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTT 235

Qy      487 CAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
            |||||||||||||||||||||||||||||||||||||||||||||
Db      234 CAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 190


RESULT 8
BF383724
LOCUS        BF383724                 594 bp    mRNA     linear    EST 27-NOV-2000
DEFINITION   602044632F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4194295 5',
             mRNA sequence.
ACCESSION    BF383724
VERSION      BF383724.1  GI:11365029
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 594)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished

```
COMMENT         Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Jeffrey E. Green, M.D.
                 cDNA Library Preparation: Life Technologies, Inc.
                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                 DNA Sequencing by: Incyte Genomics, Inc.
                 Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM9527  row: p  column: 08
                High quality sequence stop: 589.
FEATURES                    Location/Qualifiers
        source              1. .594
                            /organism="Mus musculus"
                            /mol_type="mRNA"
                            /strain="FVB/N"
                            /db_xref="taxon:10090"
                            /clone="IMAGE:4194295"
                            /lab_host="DH10B (T1 phage-resistant)"
                            /clone_lib="NCI_CGAP_Li9"
                            /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                            Average insert size 1.9 kb. Constructed by Life
                            Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT        175 a     162 c     142 g     115 t
ORIGIN
```

```
  Query Match              80.1%;  Score 431.8;  DB 10;  Length 594;
  Best Local Similarity    92.4%;  Pred. No. 8.5e-91;
  Matches  465;  Conservative    0;  Mismatches    37;  Indels    1;  Gaps    1;


Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           ||||||||||||| |||||||||||||||||||||| |||||||||||||||||||||||
Db      93 GGACCAGAGACCC-TTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 151


Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           |||||.|||||||||||||||||||||||||||| ||||||||||||||||||||||| |||
Db     152 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 211


Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           || |||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db     212 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 271


Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           |||| ||      |||||||||| |||| || || ||||| |||||||||||||||||||
Db     272 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 331


Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           ||||||||||||||||||||||||| | ||||||||||| ||||||||| |||||||||||
Db     332 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 391


Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     392 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 451


Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           |||||||||||||||||||||| ||| |||||||||||| |||||||| ||||||||||
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```
Db      452  CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 511

Qy      421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
             ||||||||||||||||||||||||||||| |||||||| ||||||| ||||||| ||| |||||
Db      512  CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 571

Qy      481  TCATTTCAGAGATGGGCATTTCC 503
             |||| || |||||||||||| ||
Db      572  ACATTACAAAGATGGGCATTGCC 594
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RESULT 9
AI119218

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LOCUS       AI119218                816 bp    mRNA      linear    EST 02-SEP-1998
DEFINITION  ue94h02.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
            IMAGE:1498803 5' similar to gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AI119218
VERSION     AI119218.1  GI:3519542
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 816)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished
  COMMENT   Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:936407
            Seq primer: custom primer used
            High quality sequence stop: 473.
FEATURES             Location/Qualifiers
     source          1. .816
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1498803"
                     /dev_stage="embryo, 14 dpc"
                     /lab_host="DH10B"
                     /clone_lib="Sugano mouse embryo mewa"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTTT];
```

double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAAGCTGCG and 3' end primer
CGACCTGCAGCTCGAGCACA."
BASE COUNT       230 a    219 c    172 g    187 t       8 others
ORIGIN

   Query Match              78.9%;  Score 425.2;  DB 9;   Length 816;
   Best Local Similarity    90.7%;  Pred. No. 3.2e-89;
   Matches  448; Conservative    0; Mismatches   46; Indels    0; Gaps    0;

Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     323 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 382

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||| |||
Db     383 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 442

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           || |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     443 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 502

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           |||| ||     |||||||||| |||| || || |||| ||||||||||||||||||||
Db     503 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 562

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           |||||||||||||||||||||||||| | ||||||||||| |||||||| ||||||||||
Db     563 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 622

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
           ||||||||||||||||||| |||||||||||||||||||||||||| ||||||||||||
Db     623 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCANGAAACAAGACCTA 682

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||||||||| ||||||||| || ||| ||||| ||||||| |||||||| ||||||||||
Db     683 CAGAATGTANGAGGAGCCTNCCACGGAGCAGAANATGCCACATCACCGCANGATCCTTTG 742

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
           |||||||||||||||||||| |||||||| ||||||| ||||||| ||   || ||| ||||
Db     743 CTGCTTGAGCAACCTGCANAACATCGAAACACCTACCAAATAACATNTATAAGTCCAATN 802

Qy     481 TCATTTCAGAGATG 494
           |||| | |||||
Db     803 ACATTACCAAGATG 816


RESULT 10
AW495481/c
LOCUS        AW495481                    499 bp     mRNA     linear    EST 24-FEB-2000

```
DEFINITION  UI-M-BH3-auy-g-11-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
            UI-M-BH3-auy-g-11-0-UI 3', mRNA sequence.
ACCESSION   AW495481
VERSION     AW495481.1  GI:7065762
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized pineal glands library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
            clones from RESEARCH GENETICS. It should be noted that Bento Soares
            is generating a small number of additional specialized
            non-redundant arrays of BMAP cDNAs whose availability will be
            considered under appropriate and limited collaborative arrangements
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..499
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH3-auy-g-11-0-UI"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NIH_BMAP_M_S4"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S4 library is a subtracted library of a series,
                     ultimately derived from a mixture of individually tagged
                     normalized libraries from  ten regions of the mouse brain
                     (cerebellum, brain stems, olfactory  bulbs, hypothalamus,
                     cortex, amygdala, basal ganglia, pineal gland,  striatum,
                     hipoccampus) after a series of subtractions to reduce the
                     representation of cDNAs from which ESTs had already been
                     generated. The following serially subtracted libraries
                     were generated in this process: NIH_BMAP_M_S4,
```

NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1.  The subtracted library
(NIH_BMAP_M_S4) was constructed as follows:  PCRamplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as  a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of  single-stranded circles.  The
remaining single-stranded circles  (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B  bacteria (LifeTechnologies) to generate the
NIH_BMAP_M_S4 library.  This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=NIH_BMAP_M_S4
TAG_TISSUE=pineal-glands
TAG_SEQ=CAGAC"
BASE COUNT        86 a     112 c     124 g     177 t
ORIGIN

  Query Match              78.5%;  Score 423;  DB 9;  Length 499;
  Best Local Similarity    91.8%;  Pred. No. 9.5e-89;
  Matches  447;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy        50 TGTGTGGACCAAGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGA 109
             ||||||||||| ||||||||||||||||||||||||||| ||||||||||||||||||||
Db       499 TGTGTGGACCGAGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGA 440

Qy       110 GGGCACCACAGACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGC 169
             ||||||| |||||| |||||||||||||||||||||||||||||||||||||||||||| |
Db       439 GGGCACCTCAGACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGAC 380

Qy       170 TGGAGATGTACTGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGC 229
             |||||||||||||| ||         |||||||||| |||| || || ||||| |||||||
Db       379 TGGAGATGTACTGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGC 320

Qy       230 GCCACACTGACATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGA 289
             ||||||||||||||||||||||||||||||||||||| | ||||||||||| |||||||| ||
Db       319 GCCACACTGACATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGA 260

Qy       290 AGCTGCAAAGGAGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGA 349
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       259 AGCTGCAAAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGA 200

Qy       350 AACAAGACCTACAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGC 409
             |||||||||||||||||||||||||||||||||||| ||| ||||||||||| |||||||
Db       199 AACAAGACCTACAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGC 140

Qy       410 AAGATCCTTTGCTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAA 469
             | |||||||||||||||||||||||||||||||||||||| |||||||| |||||||| ||||||
Db       139 AGGATCCTTTGCTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAA 80

Qy       470 TGAGTTCAATATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATT 529
             | ||| ||||| |||| || ||||||||||||| |||||||||| ||||||||||||||||
Db        79 TAAGTCCAATAACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATT 20

```
Qy        530 CCCGGAA 536
              ||   ||
Db         19 CCAAAAA 13
```

RESULT 11
AI876493/c
LOCUS       AI876493                642 bp     mRNA     linear   EST 21-JUL-1999
DEFINITION  uj59b10.x1 Sugano mouse liver mlia Mus musculus cDNA clone
            IMAGE:1924219 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH
            FACTOR IA PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AI876493
VERSION     AI876493.1  GI:5550542
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:980511
            Seq primer: custom primer used
            High quality sequence stop: 257.
FEATURES             Location/Qualifiers
     source          1..642
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1924219"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="Sugano mouse liver mlia"
                     /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
                     (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert.  Size selection was

BASE COUNT        127 a      154 c     175 g     185 t        1 others
ORIGIN

  Query Match             78.1%;  Score 421.2;  DB 9;   Length 642;
  Best Local Similarity   91.1%;  Pred. No. 2.6e-88;
  Matches  458;  Conservative    0;  Mismatches   44;  Indels    1;  Gaps   1;

Qy       2 GACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCAA 61
           |||||||||||||||||||||||||||||||||||||| ||||||||| |||||||||||| |
Db     503 GACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGGTCGTGTGTGGACCGA 444

Qy      62 GGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAGA 121
           ||||||||| |||||||||| |||||| ||||||||||||||| ||||||||||| ||||
Db     443 GGGGCTTTTTCTTCAACAAGGCCACAGGCTATGGCTCCAGCATTTGGAGGGCACCTCAGA 384

Qy     122 CGGGCATTGTGGATGAGTGTTGCTTCCGG-AGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           | |  || ||||||||||||||||||||| ||||||||||||| || ||| ||||||||
Db     383 CAGTCAATGTGGATGAGTGTTGCTTCCGGAAGCTGTGATCTGAGAAGACTGNAGATGTAC 324

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           |||| ||       ||||||||||  |||| || || ||||| ||||||||||||||||||
Db     323 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 264

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           |||||||||||||||||||||||| | ||||||||||| ||||||||| |||||||||||||
Db     263 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 204

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
           ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db     203 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 144

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||||||||||||||||||||||| ||| |||||||||||||| |||||||| |||||||||
Db     143 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 84

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
           ||||||||||||||||||||||||||||| ||||||| ||||||| ||||||| ||| |||||
Db      83 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 24

Qy     481 TCATTTCAGAGATGGGCATTTCC 503
           ||||| || |||||||||||||||
Db      23 ACATTACAAAGATGGGCATTTCC 1


RESULT 12
AA963258/c
LOCUS       AA963258               525 bp    mRNA    linear   EST 09-MAR-1999
DEFINITION  UI-R-E1-gh-f-04-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone
            UI-R-E1-gh-f-04-0-UI 3', mRNA sequence.
ACCESSION   AA963258
VERSION     AA963258.1  GI:4278182
KEYWORDS    EST.

```
SOURCE          Rattus norvegicus (Norway rat)
  ORGANISM      Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
REFERENCE       1  (bases 1 to 525)
  AUTHORS       Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE         Normalization and subtraction: two approaches to facilitate gene
                discovery
  JOURNAL       Genome Res. 6 (9), 791-806 (1996)
  MEDLINE       97044477
   PUBMED       8889548
COMMENT         On May 18, 1998 this sequence version replaced gi:3136750.
                Contact: Soares, MB
                Coordinated Laboratory for Computational Genomics
                University of Iowa
                375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
                Tel: 319 335 8250
                Fax: 319 335 9565
                Email: bento-soares@uiowa.edu
                The sequence tag present in the cDNA between the NotI site and the
                oligo-dT track served to identify it as a clone from the normalized
                adult 12-Day-Embryo library. cDNA Library Preparation: M. Fatima
                Bonaldo, Ph.D. Clone distribution: clones will be available through
                Research Genetics
                Seq primer: M13 Forward.
FEATURES                 Location/Qualifiers
     source              1. .525
                         /organism="Rattus norvegicus"
                         /mol_type="mRNA"
                         /strain="Sprague-Dawley"
                         /db_xref="taxon:10116"
                         /clone="UI-R-E1-gh-f-04-0-UI"
                         /dev_stage="adult"
                         /lab_host="DH10B (Life Technologies)"
                         /clone_lib="UI-R-E1"
                         /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                         polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-E1
                         library is a subtracted library derived from the UI-R-E0
                         library.  The UI-R-E0 library  consisted of a mixture of
                         individually  tagged normalized libraries constructed from
                         8, 12 and 18-day embryo.  The tag is a string of 3-5
                         nucleotides present between the Not I site  and the
                         oligo-dT track which allows identification of the library
                         of  origin of a clone within the mixture.  The subtracted
                         library (UI-R-E1) was constructed as follows: PCR
                         amplified cDNA inserts from a pool of  UI-R-E0 clones from
                         which 3' ESTs had been derived was used as a driver in a
                         hybridization with the UI-R-E0 library in the form of
                         single-stranded circles. The remaining single-stranded
                         circles (subtracted library) was purified by
                         hydroxyapatite column chromatography, converted to
                         double-stranded circles and electroporated into DH10B
                         bacteria (Life Technologies) to generate the UI-R-E1
                         library. This procedure has been previously described
                         (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                         1996)"
```

BASE COUNT        107 a      133 c       126 g       159 t
ORIGIN

   Query Match               74.7%;   Score 402.6;   DB 9;   Length 525;
   Best Local Similarity     88.5%;   Pred. No. 5.8e-84;
   Matches  470;  Conservative     0;  Mismatches     9;  Indels   52;  Gaps      1;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      521 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 462

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db      461 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 402

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      401 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 342

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            ||||   |         |||||||||||||||||||||||||||||||||||||||||||
Db      341 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 282

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            |||||||||||||||
Db      281 ATGCCCAAGACTCAG--------------------------------------------- 267

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      266 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 214

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      213 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 154

Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      153 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 94

Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       93 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 43


RESULT 13
AA945553/c
LOCUS        AA945553                500 bp     mRNA      linear     EST 08-JAN-1999
DEFINITION   EST201052 Normalized rat liver, Bento Soares Rattus sp. cDNA clone
             RLIAO83 3' end, mRNA sequence.
ACCESSION    AA945553
VERSION      AA945553.1  GI:4132547
KEYWORDS     EST.
SOURCE       Rattus sp.
  ORGANISM   Rattus sp.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
             Rattus.

```
REFERENCE     1  (bases 1 to 500)
  AUTHORS     Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
              Kerlavage,A.R. and Adams,M.D.
   TITLE      Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
              Gene Index
  JOURNAL     Unpublished
  COMMENT     On May 1, 1998 this sequence version replaced gi:3105469.
              Contact: Lee, NH
              The Institute for Genomic Research
              9712, Medical Center Drive, Rockville, MD 20850, USA
              Tel: (301)-838-3529
              Fax: (301)-838-0208
              Email: nhlee@tigr.org
              Seq primer: M13-21.
  FEATURES             Location/Qualifiers
       source          1. .500
                       /organism="Rattus sp."
                       /mol_type="mRNA"
                       /db_xref="taxon:10118"
                       /clone="RLIAO83"
                       /clone_lib="Normalized rat liver, Bento Soares"
                       /note="Organ: liver; Vector: pT7T3Pac; Site_1: EcoRI;
                       Site_2: NotI"
BASE COUNT        99 a     129 c     130 g     142 t
ORIGIN

   Query Match              74.5%;  Score 401.6;  DB 9;  Length 500;
   Best Local Similarity    88.5%;  Pred. No. 9.8e-84;
   Matches  469;  Conservative    0;  Mismatches    9;  Indels   52;  Gaps    1;


Qy         1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       478 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 419


Qy        61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       418 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 359


Qy       121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       358 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 299


Qy       181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
             ||||  |        |||||||||||||||||||||||||||||||||||||||||||||
Db       298 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 239


Qy       241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
             ||||||||||||||||
Db       238 ATGCCCAAGACTCAG----------------------------------------------- 224


Qy       301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       223 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 171


Qy       361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
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Db       170 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 111
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Qy      421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
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Db      110  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 51


Qy      481  TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
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Db       50  CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 1
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RESULT 14
AI599751/c
LOCUS       AI599751                  525 bp     mRNA      linear    EST 21-APR-1999
DEFINITION  EST251454 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
            REMEG86 3' end, mRNA sequence.
ACCESSION   AI599751
VERSION     AI599751.1  GI:4608799
KEYWORDS    EST.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
  TITLE     Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            Seq primer: M13-21.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Rattus sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:10118"
                     /clone="REMEG86"
                     /dev_stage="embryo 8, 12, 18 dpc"
                     /clone_lib="Normalized rat embryo, Bento Soares"
                     /note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT      107 a     133 c     140 g     145 t
ORIGIN

  Query Match             74.1%;  Score 399.4;  DB 9;  Length 525;
  Best Local Similarity   88.1%;  Pred. No. 3.2e-83;
  Matches  468;  Conservative   0;  Mismatches   11;  Indels   52;  Gaps    1;

Qy        1  GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      480  GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAATTCGTGTGTGGACCA 421

Qy       61  AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
```

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             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     420  AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 361

Qy     121  ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360  ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 301

Qy     181  TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
             ||||  |       ||||||||||||||||||||||||||||||||||||||||| ||||
Db     300  TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACATTGAC 241

Qy     241  ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
             ||||||||||||||||
Db     240  ATGCCCAAGACTCAG--------------------------------------------- 226

Qy     301  AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     225  -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 173

Qy     361  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 113

Qy     421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
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Db     112  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 53

Qy     481  TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
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Db      52  CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 2
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RESULT 15
BI294072/c
LOCUS       BI294072                 499 bp    mRNA    linear    EST 19-JUL-2001
DEFINITION  UI-R-DK0-cej-b-03-0-UI.s1 UI-R-DK0 Rattus norvegicus cDNA clone
            UI-R-DK0-cej-b-03-0-UI 3', mRNA sequence.
ACCESSION   BI294072
VERSION     BI294072.1  GI:14956179
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250

Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized rat heart pool library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.

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FEATURES              Location/Qualifiers
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                      /organism="Rattus norvegicus"
                      /mol_type="mRNA"
                      /strain="Sprague-Dawley"
                      /db_xref="taxon:10116"
                      /clone="UI-R-DK0-cej-b-03-0-UI"
                      /dev_stage="ADULT"
                      /lab_host="DH10B (Life Technologies)"
                      /clone_lib="UI-R-DK0"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DK0
                      library is a subtracted library derived from a mixture of
                      five individually tagged normalized rat libraries:
                      brain-nRBP (20%), heart-nRHP (20%), kidney-nRKP (20%),
                      aorta-nRAP (20%), and placenta-nRPP (20%). Each original
                      library was constructed from a mixture of equal amounts of
                      RNA from seven different developmental time-points:
                      embryonic day 17, embryonic day 19, embryonic day 21,
                      adult day 1, adult day 12, adult day 75, and adult day
                      200. (Exception: the aorta pool does not contain embryonic
                      day 17 RNA and the placenta pool contains only the three
                      embryonic stages). Each library was normalized
                      individually according to the procedure described by
                      Bonaldo, Lennon & Soares (Genome Research Genome 6:
                      791-806, 1996). For construction of the DK0 subtracted
                      library, plasmid DNA from each of the five individually
                      tagged normalized libraries was mixed in the proportions
                      specified above and electroporated into competent bacteria
                      for production of single-stranded circular DNA
                      representing the pool of libraries. Single-stranded
                      circular DNA representing these five normalized libraries
                      was then used as a tracer in a subtractive hybridization
                      with a driver (PCR amplified inserts from a plasmid DNA
                      template preparation) comprising: a) a set of about 1,000
                      arrayed clones from each of the five non-normalized
                      libraries of brain (CT0s), heart (CS0s), kidney (CU0s),
                      aorta (CW0s), and placenta (CX0s). The resulting pool of
                      approximately 5,000 clones represented about 33.3% of the
                      final driver population. A set of about 2,000 arrayed
                      clones from each of the five normalized libraries of brain
                      (CT0), heart (CS0), kidney (CU0), aorta (CW0), and
                      placenta (CX0). The resulting pool of about 10,000 clones
                      represented about 66.6% of the final driver population.
                      TAG_LIB=UI-R-DK0
```

```
                    TAG_TISSUE=rat heart pool
                    TAG_SEQ=ATAAGATAAC"
BASE COUNT        97 a      124 c      121 g      156 t        1 others
ORIGIN
                                                                              \
  Query Match              73.3%;   Score 395;   DB 12;   Length 499;
  Best Local Similarity    88.0%;   Pred. No. 3.4e-82;
  Matches  463;   Conservative    0;   Mismatches   11;   Indels   52;   Gaps    1;


Qy         6 AGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCAAGGGG 65
             ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       499 AGAGACCCTNTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCAAGGGG 440


Qy        66 CTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAGACGGG 125
             ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       439 CTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAGACGGG 380


Qy       126 CATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGT 185
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       379 CATTGTGGATGAGTGTTGCTTCCGGAGCTGTTATCTGAGGAGGCTGGAGATGTACTGTGC 320


Qy       186 CCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACATGCC 245
                |       |||||||||||||||||||||||||||||||||||||||||||||||||
Db       319 TCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACATGCC 260


Qy       246 CAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAG 305
             ||||||||||
Db       259 CAAGACTCAG--------------------------------------------------- 250


Qy       306 GAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAA 365
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       249 --AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAA 192


Qy       366 TGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCTGCT 425
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       191 TGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCTGCT 132


Qy       426 TGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATATCATT 485
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Db       131 TGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATT 72


Qy       486 TCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
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Db        71 TCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 26


Search completed: December 13, 2003, 07:29:50
Job time : 1758.93 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003   Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          December 13, 2003, 05:41:20 ; Search time 2408.26 Seconds
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Title:           US-09-852-261-3
Perfect score:   539
Sequence:        1 ggaccagagaccctttgcgg..........agtaaacattcccggaattc 539

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters:      5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 539 | 100.0 | 539 | 6 | AX147744 | AX147744 Sequence |
| 2 | 539 | 100.0 | 539 | 6 | AX300781 | AX300781 Sequence |
| 3 | 535.8 | 99.4 | 710 | 10 | RATIGFIA | M15480 Rat insulin |
| 4 | 516.6 | 95.8 | 798 | 10 | RNIGFI2 | X06108 Rat mRNA (c |
| 5 | 516.6 | 95.8 | 958 | 10 | RNIGFI1 | X06107 Rat mRNA (c |
| 6 | 470.2 | 87.2 | 1536 | 10 | BC012409 | BC012409 Mus muscu |
| 7 | 453.8 | 84.2 | 651 | 10 | MMIGFIBR | X04482 Mouse mRNA |
| 8 | 425 | 78.8 | 487 | 6 | AX147752 | AX147752 Sequence |
| 9 | 425 | 78.8 | 487 | 6 | AX300789 | AX300789 Sequence |
| 10 | 421.8 | 78.3 | 1346 | 10 | RATIGFIB | M15481 Rat insulin |
| 11 | 402.6 | 74.7 | 1052 | 10 | RATIGF1A | D00698 Rattus sp. |
| 12 | 401 | 74.4 | 513 | 26 | RNMGJIL | M17714 Rat insulin |
| 13 | 401 | 74.4 | 521 | 10 | RNIGFIR | X06043 Rattus norv |
| 14 | 387 | 71.8 | 826 | 10 | RATIGFIAA | M17335 Rat insulin |
| 15 | 361.6 | 67.1 | 696 | 10 | MMIGFIAR | X04480 Mouse mRNA |
| 16 | 356.8 | 66.2 | 523 | 6 | AX147746 | AX147746 Sequence |
| 17 | 356.8 | 66.2 | 523 | 6 | AX300783 | AX300783 Sequence |
| 18 | 325.2 | 60.3 | 517 | 6 | AX147742 | AX147742 Sequence |
| 19 | 325.2 | 60.3 | 517 | 6 | AX300779 | AX300779 Sequence |
| 20 | 299.6 | 55.6 | 671 | 6 | AX526045 | AX526045 Sequence |
| 21 | 274.2 | 50.9 | 7260 | 6 | AX375028 | AX375028 Sequence |
| 22 | 274.2 | 50.9 | 7260 | 6 | AX411095 | AX411095 Sequence |
| 23 | 274.2 | 50.9 | 7260 | 9 | HSIGFACI | X57025 Human IGF-I |
| 24 | 272.6 | 50.6 | 666 | 6 | A29119 | A29119 H.sapiens I |
| 25 | 272.6 | 50.6 | 725 | 9 | HSIGFI | X00173 Homo sapien |
| 26 | 272.6 | 50.6 | 728 | 9 | HUMGFII | M29644 Human insul |
| 27 | 271.2 | 50.3 | 616 | 9 | HSIGF1A | X56773 H.sapiens m |
| 28 | 271 | 50.3 | 620 | 6 | I08370 | I08370 Sequence 2 |
| 29 | 270 | 50.1 | 1076 | 9 | HUMIGFI | M27544 Human insul |
| 30 | 268.8 | 49.9 | 444 | 9 | HSU40870 | U40870 Human alter |
| 31 | 267.2 | 49.6 | 432 | 4 | AF022961 | AF022961 Oryctolag |
| 32 | 262 | 48.6 | 471 | 6 | AX147754 | AX147754 Sequence |
| 33 | 262 | 48.6 | 471 | 6 | AX300791 | AX300791 Sequence |

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34      260     48.2    567  4    PIGGFIIA              M31175 Pig insulin
35      258     47.9    532  4    SSILGF1M              X17492 Porcine mRN
36      237.4   44.0    888  4    ECU85272              U85272 Equus cabal
37      231     42.9    730  9    HSIGF1B               X56774 H.sapiens m
38      231     42.9   1094  9    HUMGFIB               M11568 Human insul
39      231     42.9   1136  6    E01349                E01349 cDNA encodi
40      231     42.9   1136  6    I08009                I08009 Sequence 3
41      230.2   42.7    978  4    GOTIGFI               D11378 Goat mRNA f
42      230.2   42.7    978  6    E05279                E05279 DNA encodin
43      229.2   42.5    384  10   AF440694              AF440694 Mus muscu
44      228.6   42.4    836  10   CPIGF1                X52951 Guinea pig
45      228.6   42.4   1284  4    BTILGF1A              X15726 Bovine mRNA
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ALIGNMENTS


RESULT 1
AX147744

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LOCUS       AX147744                  539 bp     DNA       linear    PAT 31-AUG-2001
DEFINITION  Sequence 3 from Patent WO0136483.
ACCESSION   AX147744
VERSION     AX147744.1  GI:14346789
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Goldspink,G.R. and Johnson,I.R.
  TITLE     Use of the insulin-like-growth factor i isoform mgf for the
            treatment of neurological disorders
  JOURNAL   Patent: WO 0136483-A 3 25-MAY-2001;
            University College London (GB)
FEATURES             Location/Qualifiers
     source          1..539
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
     CDS             <1..336
                     /note="unnamed protein product"
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                     /translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV
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                     KGSTLEEHK"
BASE COUNT       161 a    136 c     139 g     103 t
ORIGIN
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   Query Match            100.0%;  Score 539;  DB 6;  Length 539;
   Best Local Similarity  100.0%;  Pred. No. 5.5e-157;
   Matches  539;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
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Db      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
                  |||.||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
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RESULT 2
AX300781
LOCUS          AX300781                    539 bp      DNA       linear    PAT 30-NOV-2001
DEFINITION     Sequence 3 from Patent WO0185781.
ACCESSION      AX300781
VERSION        AX300781.1  GI:17382062
KEYWORDS       .
SOURCE         Rattus sp.
  ORGANISM     Rattus sp.
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE      1
  AUTHORS      Goldspink,G.D. and Terenghi,G.B.
  TITLE        Repair of nerve damage
  JOURNAL      Patent: WO 0185781-A 3 15-NOV-2001;
               University College London (GB) ; East Grinstead Medical Research
               Trust (GB)
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Rattus sp."

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                         /mol_type="genomic DNA"
                         /db_xref="taxon:10118"
            CDS          <1..336
                         /note="unnamed protein product"
                         /codon_start=1
                         /protein_id="CAD13041.1"
                         /db_xref="GI:17382063"
                         /translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV
                         DECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRR
                         KGSTLEEHK"
BASE COUNT        161 a     136 c      139 g      103 t
ORIGIN
```

```
   Query Match                100.0%;  Score 539;  DB 6;  Length 539;
   Best Local Similarity   100.0%;  Pred. No. 5.5e-157;
   Matches  539;  Conservative   0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy     481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
```

RESULT 3
RATIGFIA
LOCUS        RATIGFIA                  710 bp     mRNA     linear    ROD 27-APR-1993

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DEFINITION   Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
ACCESSION    M15480
VERSION      M15480.1  GI:204749
KEYWORDS     growth factor; insulin-like growth factor.
SOURCE       Rattus norvegicus (Norway rat)
  ORGANISM   Rattus norvegicus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
             Rattus.
REFERENCE    1  (bases 1 to 710)
  AUTHORS    Roberts,C.T. Jr., Lasky,S.R., Lowe,W.L. Jr., Seaman,W.T. and
             LeRoith,D.
  TITLE      Molecular cloning of rat insulin-like growth factor I complementary
             deoxyribonucleic acids: differential messenger ribonucleic acid
             processing and regulation by growth hormone in extrahepatic tissues
  JOURNAL    Mol. Endocrinol. 1 (3), 243-248 (1987)
  MEDLINE    88288198
   PUBMED    3453891
COMMENT      Original source text: Rat (Sprague-Dawley) adult liver cDNA to
             mRNA, clone pRIGF-1-42.
             Draft entry and computer-readable copy of sequence in [Mol.
             Endocrinol. (1987) In press] kindly
             provided by S.R.Lasky, 16-MAR-1987.
FEATURES             Location/Qualifiers
     source          1. .710
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
     CDS             106. .507
                     /note="insulin-like growth factor precursor"
                     /codon_start=1
                     /protein_id="AAA41385.1"
                     /db_xref="GI:204750"
                     /translation="MSSSHLFYLALCLLTFTSSATAGPETLCGAELVDALQFVCGPRG
                     FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTD
                     MPKTQKSQPLSTHKKRKLQRRRKGSTLEEHK"
     sig_peptide     106. .171
                     /note="insulin-like growth factor signal peptide"
     mat_peptide     172. .258
                     /product="insulin-like growth factor B peptide"
     mat_peptide     259. .294
                     /product="insulin-like growth factor C peptide"
     mat_peptide     295. .357
                     /product="insulin-like growth factor A peptide"
     mat_peptide     358. .381
                     /product="insulin-like growth factor D peptide"
     mat_peptide     382. .504
                     /product="insulin-like growth factor E peptide"
BASE COUNT      202 a     191 c     172 g     145 t
ORIGIN        1 bp upstream of EcoRI site.

   Query Match             99.4%;  Score 535.8;  DB 10;  Length 710;
   Best Local Similarity   99.6%;  Pred. No. 5.8e-156;
   Matches  537;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    172  GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA  231

Qy     61  AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG  120
           ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    232  AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG  291

Qy    121  ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    292  ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC  351

Qy    181  TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    352  TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC  411

Qy    241  ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    412  ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG  471

Qy    301  AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    472  AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA  531

Qy    361  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    532  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG  591

Qy    421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    592  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA  651

Qy    481  TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC  539
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    652  CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC  710
```

RESULT 4
RNIGFI2
LOCUS       RNIGFI2                     798 bp    mRNA     linear    ROD 12-SEP-1993
DEFINITION  Rat mRNA (clone IGF1AB2) for insulin-like growth factor I.
ACCESSION   X06108 M32339 Y00429
VERSION     X06108.1  GI:56426
KEYWORDS    insulin-like growth factor I.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Shimatsu,A. and Rotwein,P.
  TITLE     Sequence of Two Rat Insulin-like Growth Factor I mRNAs Differing
            Within the 5' Untranslated Region
  JOURNAL   Nucleic Acids Res. 15 (1987) In press
REFERENCE   2  (bases 1 to 798)
  AUTHORS   Rotwein,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1987) Rotwein P., Washington University, School
            of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO

COMMENT          Another IGF-I mRNA of rat liver differing in the 5' UT-region is
                 described in <X06107>.
FEATURES             Location/Qualifiers
     source          1. .798
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="liver"
     misc_feature    1. .72
                     /note="5' UT-region"
     CDS             73. .552
                     /note="IGF-I (AA 1-159)"
                     /codon_start=1
                     /protein_id="CAA29481.1"
                     /db_xref="GI:56427"
                     /translation="MGKISSLPTQLFKICLCDFLKIKIHIMSSSHLFYLALCLLTFTS
                     SATAGPETLCGAELVDALQFVCGPRGFYFNKPTGYGSSIRRAPQTGIVDECCFRSCDL
                     RRLEMYCAPLKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRRKGSTLEEHK"
     misc_feature    553. .798
                     /note="3' UT-region"
BASE COUNT      238 a    196 c    183 g    181 t
ORIGIN

  Query Match              95.8%;  Score 516.6;  DB 10;  Length 798;
  Best Local Similarity    98.3%;  Pred. No. 5.9e-150;
  Matches  522;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;


Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     217 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 276


Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     277 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 336


Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     337 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 396


Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           ||||  |||    |   |||||||||||||||||||||||||||||||||||||||||||
Db     397 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 456


Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     457 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 516


Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     517 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 576


Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     577 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 636

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Qy       421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA  480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       637  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA  696

Qy       481  TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC  531
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       697  CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC  747
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RESULT 5
RNIGFI1
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LOCUS       RNIGFI1                 958 bp    mRNA       linear    ROD 12-SEP-1993
DEFINITION  Rat mRNA (clone IGF1AB1) for insulin-like growth factor I.
ACCESSION   X06107 M32260 Y00429
VERSION     X06107.1  GI:56424
KEYWORDS    insulin-like growth factor I.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Shimatsu,A. and Rotwein,P.
  TITLE     Sequence of two rat insulin-like growth factor I mRNAs differing
            within the 5' untranslated region
  JOURNAL   Nucleic Acids Res. 15 (17), 7196 (1987)
  MEDLINE   88015572
   PUBMED   3658684
REFERENCE   2  (bases 1 to 958)
  AUTHORS   Rotwein,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1987) Rotwein P., Washington University, School
            of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO
            63110, USA
COMMENT     Another IGF-I mRNA of rat liver differing in the 5' UT-region is
            described in <X06108>.
FEATURES             Location/Qualifiers
     source          1..958
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Srpague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="liver"
     misc_feature    1..258
                     /note="5' UT-region"
     CDS             259..738
                     /note="IGF-I (AA 1-159)"
                     /codon_start=1
                     /protein_id="CAA29480.1"
                     /db_xref="GI:56425"
                     /db_xref="SWISS-PROT:P08024"
                     /translation="MGKISSLPTQLFKICLCDFLKIKIHIMSSSHLFYLALCLLTFTS
                     SATAGPETLCGAELVDALQFVCGPRGFYFNKPTGYGSSIRRAPQTGIVDECCFRSCDL
                     RRLEMYCAPLKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRRKGSTLEEHK"
     misc_feature    736..958
                     /note="3' UT-region"
BASE COUNT      260 a    246 c    209 g    243 t
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ORIGIN

Query Match          95.8%;  Score 516.6;  DB 10;  Length 958;
Best Local Similarity   98.3%;  Pred. No. 6.1e-150;
Matches   522;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 462

Qy     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    463 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 522

Qy    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 582

Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
          ||||   |      ||||||||||||||||||||||||||||||||||||||||||||||
Db    583 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 642

Qy    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 702

Qy    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 762

Qy    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 822

Qy    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 882

Qy    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 933


RESULT 6
BC012409
LOCUS       BC012409                1536 bp    mRNA    linear    ROD 16-APR-2003
DEFINITION  Mus musculus insulin-like growth factor 1, mRNA (cDNA clone
            MGC:18617 IMAGE:4194295), complete cds.
ACCESSION   BC012409
VERSION     BC012409.1  GI:15214568
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1536)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

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           Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
           Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
           Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
           Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
           Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
           Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
           Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
           Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
           McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
           Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
           Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
           Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
           Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
           Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
           Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
           Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
           Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
           human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1536)
  AUTHORS   Strausberg,R.
   TITLE    Direct Submission
  JOURNAL   Submitted (15-AUG-2001) National Institutes of Health, Mammalian
           Gene Collection (MGC), Cancer Genomics Office, National Cancer
           Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
           USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
 COMMENT    Contact: MGC help desk
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Jeffrey E. Green, M.D.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Baylor College of Medicine Human Genome
           Sequencing Center
           Center code: BCM-HGSC
           Web site: http://www.hgsc.bcm.tmc.edu/cdna/
           Contact: amg@bcm.tmc.edu
           Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
           Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
           A.N., Gibbs, R.A.

           Clone distribution: MGC clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           Series: IRAK Plate: 24 Row: k Column: 11
           This clone was selected for full length sequencing because it
           passed the following selection criteria: matched mRNA gi: 6754307.
FEATURES             Location/Qualifiers
     source          1. .1536
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="MGC:18617 IMAGE:4194295"
                     /tissue_type="Liver, normal. 5 month old male mouse."
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  Query Match              87.2%;  Score 470.2;  DB 10;  Length 1536;
  Best Local Similarity    92.8%;  Pred. No. 2.1e-135;
  Matches  493; Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;


Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       94 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 153

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |||
Db      154 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 213

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db      214 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 273

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            |||| ||         |||||||||| |||| || || ||||| ||||||||||||||||
Db      274 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 333

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            |||||||||||||||||||||||| | ||||||||| ||||||||| |||||||||||||
Db      334 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 393

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
            ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db      394 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 453

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            ||||||||||||||||||||||| ||| ||||||||||||| |||||||| ||||||||||
Db      454 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 513

Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            ||||||||||||||||||||||||||| ||||||| ||||||| ||||||| ||| |||||
Db      514 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 573

Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
            |||| || ||||||||||||||| |||||||||| |||||||||||||||||
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Db        574 ACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATTCC 624


RESULT 7
MMIGFIBR
LOCUS         MMIGFIBR              651 bp    mRNA    linear    ROD 21-MAR-1995
DEFINITION    Mouse mRNA for preproinsulin-like growth factor IB.
ACCESSION     X04482
VERSION       X04482.1  GI:51806
KEYWORDS      growth factor; insulin-like growth factor IB; preproinsulin-like
              growth factor IB; signal peptide.
SOURCE        Mus musculus (house mouse)
  ORGANISM    Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1  (bases 1 to 651)
  AUTHORS     Bell,G.I., Stempien,M.M., Fong,N.M. and Rall,L.B.
  TITLE       Sequences of liver cDNAs encoding two different mouse insulin-like
              growth factor I precursors
  JOURNAL     Nucleic Acids Res. 14 (20), 7873-7882 (1986)
  MEDLINE     87040760
   PUBMED     3774549
COMMENT       The sequence is identical to the preproIGF-IA sequence (X04480)
              except for the presence of a 52 bp insertion following codon 86
              (position 397 to 448), caused by alternative RNA splicing. The B
              domain of IGF comprises residues 1-29 (position 139-225), the C
              domain residues 30-41 (position 226-261), the A domain residues
              42-62 (position 262-324) and the D domain residues 63-70 (position
              325-348).
FEATURES             Location/Qualifiers
     source          1. .651
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="Balb/c"
                     /db_xref="taxon:10090"
                     /clone="migfl-4"
                     /tissue_type="liver"
     misc_feature    43. .45
                     /note="pot. translation start"
     CDS             73. .474
                     /note="prepro IGF-IB (aa -22 to 111)"
                     /codon_start=1
                     /protein_id="CAA28170.1"
                     /db_xref="GI:51807"
                     /db_xref="MGI:96432"
                     /db_xref="SWISS-PROT:P05018"
                     /translation="MSSSHLFYLALCLLTFTSSTTAGPETLCGAELVDALQFVCGPRG
                     FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPTKAARSIRAQRHTD
                     MPKTQKSPSLSTNKKTKLQRRRKGSTFEEHK"
     sig_peptide     73. .138
                     /note="signal peptide (aa -22 to -1)"
     mat_peptide     139. .348
                     /product="mature IGF-IB (aa 1-70)"
     misc_feature    349. .471
                     /note="COOH-terminal peptide (E domain) (aa 71 to 111)"
     polyA_site      651
                     /note="polyA site"

BASE COUNT      193 a      185 c      149 g      124 t
ORIGIN

  Query Match              84.2%;   Score 453.8;   DB 10;   Length 651;
  Best Local Similarity    92.8%;   Pred. No. 2.4e-130;
  Matches  476;   Conservative   0;   Mismatches   37;   Indels    0;   Gaps    0;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      139 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 198

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |||
Db      199 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 258

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            |||| || |||||||||| |||| || || ||||| ||||||||||||||||||
Db      319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 378

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            |||||||||||||||||||||||| | |||||||||| ||||||||| ||||||||||||
Db      379 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db      439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            ||||||||||||||||||||||| ||| ||||||||||||| |||||||| |||||||||
Db      499 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558

Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            ||||||||||||||||||||||||||||| |||||||| ||||||| |||||||| |||||
Db      559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618

Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAA 513
            |||| || ||||||||||||||||| ||||||||
Db      619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651


RESULT 8
AX147752
LOCUS       AX147752                487 bp    DNA       linear    PAT 31-AUG-2001
DEFINITION  Sequence 11 from Patent WO0136483.
ACCESSION   AX147752
VERSION     AX147752.1  GI:14346797
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1

FEATURES                Location/Qualifiers
     source             1. .487
                        /organism="Rattus norvegicus"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:10116"
     CDS                <1. .318
                        /note="unnamed protein product"
                        /codon_start=1
                        /protein_id="CAC41179.1"
                        /db_xref="GI:14346798"
                        /db_xref="REMTREMBL:CAC41179"
                        /translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV
                        DECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTDMPKTQKEVHLKNTSRGSAGNKT
                        YRM"
BASE COUNT      139 a      123 c      126 g       99 t
ORIGIN

  Query Match                78.8%;   Score 425;   DB 6;   Length 487;
  Best Local Similarity   90.4%;   Pred. No. 2.3e-121;
  Matches  487;  Conservative     0;  Mismatches     0;  Indels   52;  Gaps    1;

Qy      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
          |||||||||||||||
Db    241 ATGCCCAAGACTCAG--------------------------------------------- 255

Qy    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    256 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 308

Qy    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 368

Qy    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 428

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Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      429 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 487
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RESULT 9
AX300789
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LOCUS       AX300789                487 bp    DNA      linear    PAT 30-NOV-2001
DEFINITION  Sequence 11 from Patent WO0185781.
ACCESSION   AX300789
VERSION     AX300789.1  GI:17382070
KEYWORDS    .
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Goldspink,G.D. and Terenghi,G.B.
  TITLE     Repair of nerve damage
  JOURNAL   Patent: WO 0185781-A 11 15-NOV-2001;
            University College London (GB) ; East Grinstead Medical Research
            Trust (GB)
FEATURES             Location/Qualifiers
     source          1. .487
                     /organism="Rattus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10118"
     CDS             <1. .318
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD13044.1"
                     /db_xref="GI:17382071"
                     /translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV
                     DECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTDMPKTQKEVHLKNTSRGSAGNKT
                     YRM"
BASE COUNT       139 a    123 c    126 g     99 t
ORIGIN
```

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  Query Match          78.8%;  Score 425;  DB 6;  Length 487;
  Best Local Similarity 90.4%;  Pred. No. 2.3e-121;
  Matches  487;  Conservative   0;  Mismatches    0;  Indels  52;  Gaps    1;
```

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Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
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                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy      241  ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
                    ||||||||||||||||
Db      241  ATGCCCAAGACTCAG--------------------------------------------- 255

Qy      301  AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      256  -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 308

Qy      361  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      309  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 368

Qy      421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      369  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 428

Qy      481  TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      429  TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 487


RESULT 10
RATIGFIB
LOCUS       RATIGFIB                1346 bp    mRNA     linear    ROD 27-APR-1993
DEFINITION  Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
ACCESSION   M15481
VERSION     M15481.1  GI:204753
KEYWORDS    growth factor; insulin-like growth factor.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Roberts,C.T. Jr., Lasky,S.R., Lowe,W.L. Jr., Seaman,W.T. and
            LeRoith,D.
  TITLE     Molecular cloning of rat insulin-like growth factor I complementary
            deoxyribonucleic acids: differential messenger ribonucleic acid
            processing and regulation by growth hormone in extrahepatic tissues
  JOURNAL   Mol. Endocrinol. 1 (3), 243-248 (1987)
  MEDLINE   88288198
   PUBMED   3453891
COMMENT     Original source text: Rat (Sprague-Dawley) adult liver, cDNA to
            mRNA, clone pRIGF-1-25.
            Draft entry and computer-readable copy of sequence in [Mol.
            Endocrinol. (1987) In press] kindly
            provided by S.R.Lasky, 16-MAR-1987.
FEATURES             Location/Qualifiers
     source          1. .1346
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
     CDS             794. .1177
                     /note="insulin-like growth factor precursor"
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                              /codon_start=1
                              /protein_id="AAA41387.1"
                              /db_xref="GI:204754"
                              /translation="MSSSHLFYLALCLLTFTSSATAGPETLCGAELVDALQFVCGPRG
                              FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTD
                              MPKTQKEVHLKNTSRGSAGNKTYRM"
            sig_peptide       794. .859
                              /note="insulin-like growth factor signal peptide"
            mat_peptide       860. .946
                              /product="insulin-like growth factor B peptide"
            mat_peptide       947. .982
                              /product="insulin-like growth factor C peptide"
            mat_peptide       983. .1045
                              /product="insulin-like growth factor A peptide"
            mat_peptide       1046. .1069
                              /product="insulin-like growth factor D peptide"
            mat_peptide       1070. .1174
                              /product="insulin-like growth factor E peptide"
BASE COUNT        348 a      344 c      344 g      310 t
ORIGIN        1 bp upstream of EcoRI site.

  Query Match            78.3%;  Score 421.8;  DB 10;  Length 1346;
  Best Local Similarity  90.0%;  Pred. No. 2.8e-120;
  Matches  485;  Conservative   0;  Mismatches   2;  Indels  52;  Gaps    1;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      860 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 919

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db      920 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 979

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      980 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 1039

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1040 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 1099

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            ||||||||||||||||
Db     1100 ATGCCCAAGACTCAG--------------------------------------------- 1114

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1115 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 1167

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1168 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 1227

Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1228 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 1287
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Qy     481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1288 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 1346
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RESULT 11
RATIGF1A
```
LOCUS       RATIGF1A                1052 bp    mRNA     linear   ROD 29-MAY-2002
DEFINITION  Rattus sp. mRNA for insulin-like growth factor I precursor,
            complete cds.
ACCESSION   D00698
VERSION     D00698.1  GI:220780
KEYWORDS    insulin-like growth factor I.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 28 to 1052)
  AUTHORS   Shimatsu,A. and Rotwein,P.
  TITLE     Mosaic evolution of the insulin-like growth factors. Organization,
            sequence, and expression of the rat insulin-like growth factor I
            gene
  JOURNAL   J. Biol. Chem. 262 (16), 7894-7900 (1987)
  MEDLINE   87222423
   PUBMED   3034909
REFERENCE   2  (bases 1 to 1052)
  AUTHORS   Kato,H., Okoshi,A., Miura,Y. and Noguchi,T.
  TITLE     A new cDNA clone relating to larger molecular species of rat
            insulin-like growth factor-I mRNA
  JOURNAL   Agric. Biol. Chem. 54 (6), 1599-1601 (1990)
  MEDLINE   91103966
   PUBMED   1368571
COMMENT     The difference in the size of IGF-I mRNA has been suggested to be
            primarily due to differences in the 3'-untranslated region in [1].
            The cDNA clone to IGF-I mRNA reported in [2] gives direct evidence
            for this hypothesis.
FEATURES             Location/Qualifiers
     source          1. .1052
                     /organism="Rattus sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:10118"
                     /tissue_type="liver"
                     /note="788 bp upstream of AvaIII site."
     CDS             43. .426
                     /codon_start=1
                     /product="insulin-like growth factor I precursor"
                     /protein_id="BAA00604.1"
                     /db_xref="GI:220781"
                     /translation="MSSSHLFYLALCLLTFTSSATAGPETLCGAELVDALQFVCGPRG
                     FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPTKSARSIRAQRHTD
                     MPKTQKEVHLKNTSRGSAGNKTYRM"
     mat_peptide     109. .318
                     /product="insulin-like growth factor mature peptide"
     variation       606
                     /note="g in [2]; deletion in [1]"
     variation       625
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                              /note="c in [2]; a in [1]"
        variation            645
                              /note="a in [2]; deletion in [1]"
        polyA_signal         710..715
        polyA_site           731
                              /note="polyadenylation site (putative)"
        polyA_site           1023
                              /note="polyadenylation site (putative)"
BASE COUNT        301 a      256 c      225 g      270 t
ORIGIN

   Query Match              74.7%;  Score 402.6;  DB 10;  Length 1052;
   Best Local Similarity    88.5%;  Pred. No. 2.7e-114;
   Matches   470;  Conservative    0;  Mismatches    9;  Indels   52;  Gaps     1;


Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      109 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 168


Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      169 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 228


Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      229 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 288


Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            ||||   |          ||||||||||||||||||||||||||||||||||||||||||
Db      289 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 348


Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            ||||||||||||||
Db      349 ATGCCCAAGACTCAG--------------------------------------------- 363


Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      364 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 416


Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      417 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 476


Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      477 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 536


Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      537 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 587


RESULT 12
RNMGJIL
ID   RNMGJIL     standard; RNA; ROD; 513 BP.
XX
AC   M17714;
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XX
SV   M17714.1
XX
DT   01-OCT-1996 (Rel. 49, Created)
DT   04-MAR-2000 (Rel. 63, Last updated, Version 2)
XX
DE   Rat insulin-like growth factor-I mRNA, 3' end.
XX
KW   insulin-like growth factor.
XX
OS   Rattus norvegicus (Norway rat)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
XX
RN   [1]
RP   1-513
RX   MEDLINE; 87246437.
RX   PUBMED; 3595538.
RA   Murphy L.J., Bell G.I., Duckworth M.L., Friesen H.G.;
RT   "Identification, characterization, and regulation of a rat complementary
RT   deoxyribonucleic acid which encodes insulin-like growth factor-I";
RL   Endocrinology 121(2):684-691(1987).
XX
DR   GOA; P08025.
DR   SWISS-PROT; P08025; IGFA_RAT.
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .513
FT                   /db_xref="taxon:10116"
FT                   /organism="Rattus norvegicus"
FT   mRNA            <1. .513
FT                   /note="ILGF-I mRNA"
FT   sig_peptide     <1. .9
FT                   /note="insulin-like growth factor-I signal peptide"
FT   CDS             <1. .327
FT                   /codon_start=1
FT                   /db_xref="GOA:P08025"
FT                   /db_xref="SWISS-PROT:P08025"
FT                   /note="insulin-like growth factor-I precursor"
FT                   /protein_id="AAA41227.1"
FT                   /translation="ATAGPETLCGAELVDALQFVCGPRGFYFNKPTGYGSSIRRAPQTG
FT                   IVDECCFRSCDLRRLEMYCAPLKPTKSARSIRAQRHTDMPKTQKEVHLKNTSRGSAGNK
FT                   TYRM"
FT   mat_peptide     10. .324
FT                   /note="insulin-like growth factor-I"
XX
SQ   Sequence 513 BP; 143 A; 128 C; 135 G; 107 T; 0 other;
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  Query Match            74.4%;  Score 401;  DB 26;  Length 513;
  Best Local Similarity  88.3%;  Pred. No. 7.5e-114;
  Matches  469; Conservative   0; Mismatches  10; Indels  52; Gaps   1;

Qy          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGTGGACCA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGTGGACCA 69
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```
Qy     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     70 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 129

Qy    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 189

Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
          ||||   |        ||||||||||||||||||||||||||||||||||||||||||||
Db    190 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 249

Qy    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
          ||||||||||||||
Db    250 ATGCCCAAGACTCAG--------------------------------------------- 264

Qy    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 317

Qy    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 377

Qy    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378 CTGCTTGAGGAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 437

Qy    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 488


RESULT 13
RNIGFIR
LOCUS          RNIGFIR                  521 bp    mRNA    linear    ROD 31-MAR-2003
DEFINITION     Rattus norvegicus mRNA for insulin-like growth factor1 (IGF-1).
ACCESSION      X06043 M17714
VERSION        X06043.1  GI:56434
KEYWORDS       IGF-1; insulin-like growth factor I.
SOURCE         Rattus norvegicus (Norway rat)
  ORGANISM     Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE      1  (bases 1 to 521)
  AUTHORS      Murphy,L.J., Bell,G.I., Duckworth,M.L. and Friesen,H.G.
  TITLE        Identification, characterization, and regulation of a rat
               complementary deoxyribonucleic acid which encodes insulin-like
               growth factor-I
  JOURNAL      Endocrinology 121 (2), 684-691 (1987)
  MEDLINE      87246437
   PUBMED      3595538
COMMENT        On Apr 1, 2003 this sequence version replaced gi:204324.
               Data kindly reviewed (11-FEB-88) by Murphy L. J.
FEATURES             Location/Qualifiers
     source          1. .521
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                        /organism="Rattus norvegicus"
                        /mol_type="mRNA"
                        /db_xref="taxon:10116"
        CDS             <1. .327
                        /note="(AA -3 to 105)"
                        /codon_start=1
                        /product="IGF-IA precursor"
                        /protein_id="CAA29436.1"
                        /db_xref="GI:56435"
                        /db_xref="GOA:P08025"
                        /db_xref="SWISS-PROT:P08025"
                        /translation="ATAGPETLCGAELVDALQFVCGPRGFYFNKPTGYGSSIRRAPQT
                        GIVDECCFRSCDLRRLEMYCAPLKPTKSARSIRAQRHTDMPKTQKEVHLKNTSRGSAG
                        NKTYRM"
        sig_peptide     <1. .9
                        /note="insulin-like growth factor-I signal peptide"
        mat_peptide     10. .324
                        /product="insulin-like growth factor-I"
        misc_feature    10. .96
                        /note="B domain (AA 1-29)"
        misc_feature    97. .132
                        /note="C domain (AA 30-41)"
        misc_feature    133. .195
                        /note="A domain (AA 42-62)"
        misc_feature    196. .219
                        /note="D domain (AA 63-70)"
BASE COUNT        151 a     128 c     135 g     107 t
ORIGIN

   Query Match              74.4%;   Score 401;   DB 10;   Length 521;
   Best Local Similarity    88.3%;   Pred. No. 7.5e-114;
   Matches   469;   Conservative    0;   Mismatches    10;   Indels    52;   Gaps    1;

Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 69

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      70 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 129

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 189

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           ||||  |         ||||||||||||||||||||||||||||||||||||||||||||||
Db     190 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 249

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           |||||||||||||||
Db     250 ATGCCCAAGACTCAG--------------------------------------------- 264

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 317
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Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     318 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 377

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     378 CTGCTTGAGGAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 437

Qy     481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     438 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 488


RESULT 14
RATIGFIAA
LOCUS        RATIGFIAA              826 bp    mRNA    linear    ROD 27-APR-1993
DEFINITION   Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
ACCESSION    M17335
VERSION      M17335.1  GI:204751
KEYWORDS     insulin-like growth factor I.
SOURCE       Rattus norvegicus (Norway rat)
  ORGANISM   Rattus norvegicus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
             Rattus.
REFERENCE    1  (bases 1 to 826)
  AUTHORS    Casella,S.J., Smith,E.P., van Wyk,J.J., Joseph,D.R., Hynes,M.A.,
             Hoyt,E.C. and Lund,P.K.
  TITLE      Isolation of rat testis cDNAs encoding an insulin-like growth
             factor I precursor
  JOURNAL    DNA 6 (4), 325-330 (1987)
  MEDLINE    88003970
   PUBMED    3652906
COMMENT      Original source text: Rat (Sprague Dawley) testis, cDNA to mRNA,
             clone P2.
FEATURES              Location/Qualifiers
     source           1. .826
                      /organism="Rattus norvegicus"
                      /mol_type="mRNA"
                      /db_xref="taxon:10116"
        CDS           259. .642
                      /note="insulin like growth factor I"
                      /codon_start=1
                      /protein_id="AAA41386.1"
                      /db_xref="GI:204752"
                      /translation="MSSSHLFYLALCLLTFTSSATAGPETLCGAELVDALQFVCGPRG
                      FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPTKSARSIRAQRHTD
                      MPKTQKEVHLKNTSRGSAGNKTYRM"
BASE COUNT       223 a    214 c    181 g    208 t
ORIGIN

  Query Match             71.8%;  Score 387;  DB 10;  Length 826;
  Best Local Similarity   88.0%;  Pred. No. 1.9e-109;
  Matches  455;  Conservative   0;  Mismatches   10;  Indels   52;  Gaps    1;


Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
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Db     325 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAATTCGTGTGTGGACCA 384

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     385 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 444

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 504

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           ||||   |       |||||||||||||||||||||||||||||||||||||||||||||
Db     505 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 564

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           |||||||||||||||
Db     565 ATGCCCAAGACTCAG--------------------------------------------- 579

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 632

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     633 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 692

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     693 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 752

Qy     481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACA 517
           |||||||||||||||||||||||||||||||||||||
Db     753 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACA 789
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RESULT 15
MMIGFIAR
LOCUS       MMIGFIAR                696 bp     mRNA     linear    ROD 21-MAR-1995
DEFINITION  Mouse mRNA for preproinsulin-like growth factor IA.
ACCESSION   X04480
VERSION     X04480.1  GI:51801
KEYWORDS    growth factor; insulin-like growth factor IA; preproinsulin-like
            growth factor IA; signal peptide.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   Bell,G.I., Stempien,M.M., Fong,N.M. and Rall,L.B.
  TITLE     Sequences of liver cDNAs encoding two different mouse insulin-like
            growth factor I precursors
  JOURNAL   Nucleic Acids Res. 14 (20), 7873-7882 (1986)
  MEDLINE   87040760
   PUBMED   3774549
COMMENT     The B-domain of IGF-I comprises residues 1-29 (position 219-305),
            the C-domain residues 30-41 (position 306-341), the A-domain
            residues 42-62 (position 342-404) and the D-domain residues 63-70
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                        (position 405-428).
FEATURES                Location/Qualifiers
     source             1. .696
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="Balb/c"
                        /db_xref="taxon:10090"
                        /clone="migfl-2"
                        /tissue_type="liver"
     misc_feature       123. .125
                        /note="pot. translation start"
     CDS                153. .536
                        /note="put. preproIGF-IA (AA -22 to 105)"
                        /codon_start=1
                        /protein_id="CAA28168.1"
                        /db_xref="GI:51802"
                        /db_xref="MGI:96432"
                        /db_xref="SWISS-PROT:P05017"
                        /translation="MSSSHLFYLALCLLTFTSSTTAGPETLCGAELVDALQFVCGPRG
                        FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPTKAARSIRAQRHTD
                        MPKTQKEVHLKNTSRGSAGNKTYRM"
     sig_peptide        153. .218
                        /note="signal peptide (AA -22 to -1)"
     mat_peptide        219. .428
                        /product="mature IGF-IA (AA 1-70)"
     misc_feature       429. .533
                        /note="COOH-terminal peptide (E domain) (AA 71 to 105)"
     polyA_site         696
                        /note="polyA site"
BASE COUNT       201 a      200 c      148 g      147 t
ORIGIN

   Query Match              67.1%;  Score 361.6;  DB 10;  Length 696;
   Best Local Similarity    83.8%;  Pred. No. 1.6e-101;
   Matches  444;  Conservative   0;  Mismatches   34;  Indels   52;  Gaps   1;


Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db     219 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 278


Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||| |||
Db     279 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 338


Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           || |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     339 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 398


Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           |||| ||        |||||||||||  |||| || || ||||| |||||||||||||||
Db     399 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 458


Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           ||||||||||||||
Db     459 ATGCCCAAGACTCAG--------------------------------------------- 473


Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
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                      ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      474  -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 526

Qy      361  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
             ||||||||||||||||||||||||   ||| |||||||||||| |||||||| ||||||||
Db      527  CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 586

Qy      421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
             |||||||||||||||||||||||||| |||||||| |||||||| |||||||| ||| |||||
Db      587  CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 646

Qy      481  TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
             |||| || |||||||||||||| ||||||||| |||||||||||||||
Db      647  ACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATTC 696
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Search completed: December 13, 2003, 09:27:34
Job time : 2410.26 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:            December 13, 2003, 02:35:18 ; Search time 216.419 Seconds
                                                 (without alignments)
                                                 6723.048 Million cell updates/sec


Title:           US-09-852-261-3
Perfect score:   539
Sequence:        1 ggaccagagaccctttgcgg..........agtaaacattcccggaattc 539


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


Searched:        2552756 seqs, 1349719017 residues


Total number of hits satisfying chosen parameters:      5105512


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


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                 4:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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                 22:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                 23:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                 24:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                 25:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*


     Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 539 | 100.0 | 539 | 22 | AAD06399 | Rat IGF-I isoform |
| 2 | 539 | 100.0 | 539 | 24 | AAS16878 | Rat mechano-growth |
| 3 | 453.8 | 84.2 | 651 | 25 | ABV76185 | Mouse insulin-like |
| 4 | 425 | 78.8 | 487 | 22 | AAD06404 | Rat liver-type IGF |
| 5 | 425 | 78.8 | 487 | 24 | AAS16883 | Rat insulin-like g |
| 6 | 402.6 | 74.7 | 1052 | 20 | AAX27498 | Rat liver form of |
| 7 | 356.8 | 66.2 | 523 | 22 | AAD06400 | Rabbit IGF-I isofo |
| 8 | 356.8 | 66.2 | 523 | 24 | AAS16879 | Rabbit mechano-gro |
| 9 | 356.8 | 66.2 | 553 | 18 | AAT84893 | Rabbit insulin lik |
| 10 | 325.2 | 60.3 | 517 | 22 | AAD06398 | Human IGF-I isofor |
| 11 | 325.2 | 60.3 | 517 | 24 | AAS16877 | Human mechano-grow |
| 12 | 299.6 | 55.6 | 671 | 24 | ABT09479 | Phase-1 Rat CT gen |
| 13 | 274.2 | 50.9 | 818 | 8 | AAN70436 | Sequence encoding |
| 14 | 274.2 | 50.9 | 7260 | 24 | ABT11091 | Human breast cance |
| 15 | 274.2 | 50.9 | 7260 | 24 | ABK84583 | Human cDNA differe |
| 16 | 274.2 | 50.9 | 7260 | 24 | ABN97244 | Gene #3742 used to |
| 17 | 274.2 | 50.9 | 7260 | 24 | ABK64812 | Human benign prost |
| 18 | 274.2 | 50.9 | 7260 | 24 | ABK35504 | Human endometrial |
| 19 | 274.2 | 50.9 | 7260 | 24 | ABK35561 | Gene IGF1 differen |
| 20 | 272.6 | 50.6 | 777 | 18 | AAT84894 | Human insulin like |
| 21 | 271 | 50.3 | 622 | 7 | AAN60490 | Human prepro-somat |
| 22 | 262 | 48.6 | 471 | 22 | AAD06405 | Rabbit liver-type |
| 23 | 262 | 48.6 | 471 | 24 | AAS16884 | Rabbit insulin-lik |
| 24 | 231 | 42.9 | 1136 | 8 | AAN70435 | Sequence encoding |
| 25 | 230.2 | 42.7 | 978 | 14 | AAQ47804 | Sequence encoding |
| 26 | 224 | 41.6 | 612 | 22 | AAS14695 | Human cDNA encodin |
| 27 | 224 | 41.6 | 612 | 25 | ABZ83309 | Toxicologically re |
| 28 | 222 | 41.2 | 3599 | 19 | AAV50428 | Plasmid pIG0552 lo |
| 29 | 222 | 41.2 | 3599 | 19 | AAV40796 | Actual sequence of |
| 30 | 222 | 41.2 | 3600 | 19 | AAV50427 | Plasmid pIG0552 up |
| 31 | 222 | 41.2 | 3600 | 19 | AAV40795 | Expected sequence |
| 32 | 222 | 41.2 | 5707 | 20 | AAX88055 | Plasmid pIG0335 DN |
| 33 | 222 | 41.2 | 6345 | 20 | AAX88054 | Plasmid pIG0100A D |
| 34 | 213.8 | 39.7 | 286 | 25 | ABV76186 | Mouse insulin-like |
| 35 | 206.8 | 38.4 | 317 | 24 | AAS16882 | Human insulin-like |
| 36 | 206.8 | 38.4 | 318 | 22 | AAD06403 | Human liver-type I |
| 37 | 206.8 | 38.4 | 462 | 19 | AAV50426 | Human IGF-1 encodi |
| 38 | 206.8 | 38.4 | 462 | 19 | AAV40794 | Human IGF-I coding |
| 39 | 206.8 | 38.4 | 462 | 24 | ABZ35734 | Human IGF1 polynuc |
| 40 | 206.8 | 38.4 | 462 | 24 | ABX09977 | Human IGF1 DNA fra |
| 41 | 206.8 | 38.4 | 462 | 24 | ABV78158 | Human IGF1 DNA SEQ |
| 42 | 206.8 | 38.4 | 462 | 24 | ABL91699 | Human polynucleoti |
| 43 | 168.4 | 31.2 | 210 | 24 | AAD45568 | Human insulin-like |
| 44 | 168.4 | 31.2 | 210 | 24 | AAD44955 | Human insulin grow |
| 45 | 168.4 | 31.2 | 210 | 24 | ABA03146 | Native mature IGF- |

ALIGNMENTS

RESULT 1
AAD06399
ID    AAD06399 standard; cDNA; 539 BP.
XX
AC    AAD06399;
XX
DT    10-AUG-2001  (first entry)
XX
DE    Rat IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW    Rat; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW    mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW    amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW    poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW    nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW    sex-linked muscular dystrophy; peripheral neuropathy;
KW    Alzheimer's disease; Parkinson's disease; ss.
XX
OS    Rattus sp.
XX
FH    Key             Location/Qualifiers
FT    CDS             1..336
FT                    /*tag=  a
FT                    /product= "Mechano-growth factor (MGF)"
FT                    /note= "This region comprises exons 3-6. The CDS does
FT                    not include start codon"
FT                    /partial
XX
PN    WO200136483-A1.
XX
PD    25-MAY-2001.
XX
PF    15-NOV-2000; 2000WO-GB04354.
XX
PR    15-NOV-1999;   99GB-0026968.
XX
PA    (UNLO ) UNIV COLLEGE LONDON.
XX
PI    Goldspink G,  Johnson I;
XX
DR    WPI; 2001-355620/37.
DR    P-PSDB; AAE02448.
XX
PT    Use of mechano-growth factor, an isoform of Insulin-like Growth
PT    Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT    medicament for the treatment of neurological disorder -
XX
PS    Claim 4; Page 51-52; 66pp; English.
XX
CC    The present invention relates to use of mechano-growth factor (MGF),
CC    an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC    medicament for the treatment of neurological disorder. The MGF is capable
CC    of reducing motoneurone loss by 20% or greater in response to nerve
CC    avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC    rescue. The MGF polynucleotide and polypeptide are useful in the
CC    manufacture of a medicament for the treatment of a neurological disorder,

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  Query Match              100.0%;  Score 539;  DB 22;  Length 539;
  Best Local Similarity    100.0%;  Pred. No. 1.9e-142;
  Matches  539;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps    0;

Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
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Db       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy     481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
```

RESULT 2
AAS16878
ID    AAS16878 standard; cDNA; 539 BP.
XX
AC    AAS16878;
XX
DT    25-FEB-2002   (first entry)
XX
DE    Rat mechano-growth factor (MGF) cDNA.
XX
KW    Rat; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW    neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW    muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW    nerve avulsion.
XX
OS    Rattus sp.
XX
FH    Key              Location/Qualifiers
FT    CDS              1..336
FT                     /*tag=  a
FT                     /product= "Rat MGF"
FT                     /partial
FT                     /note= "No start codon"
FT    exon             1..75
FT                     /*tag=  b
FT                     /number= exon 3
FT    exon             76..258
FT                     /*tag=  c
FT                     /number= exon 4
FT    exon             259..309
FT                     /*tag=  d
FT                     /number= exon 5
FT    exon             310..333
FT                     /*tag=  e
FT                     /number= exon 6
XX
PN    WO200185781-A2.
XX
PD    15-NOV-2001.
XX
PF    10-MAY-2001; 2001WO-GB02054.
XX
PR    10-MAY-2000; 2000GB-0011278.
XX
PA    (UNLO ) UNIV COLLEGE LONDON.
PA    (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI    Goldspink G,  Terenghi G;
XX
DR    WPI; 2002-055585/07.
DR    P-PSDB; AAU10560.
XX
PT    Use of insulin-like growth factor I (IGF-I) isoform known as
PT    mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT    ability to reduce motoneuron loss in response to nerve avulsion, to
PT    treat nerve damage  -
XX

PS    Disclosure; Fig 6; 65pp; English.
XX
CC    The invention relates to the use of an insulin-like growth factor I
CC    (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC    of a medicament for treating nerve damage in the peripheral nervous
CC    system, or for treating nerve damage by localising MGF at the site of
CC    damage. The nerve damage may include severing of a nerve. The treatment
CC    may be combined with another treatment (such as a polypeptide growth
CC    factor other than MGF) that prevents or diminishes degeneration of the
CC    target organ (for example, muscle) which the damaged nerve innervates,
CC    whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC    MGF prevents or diminishes degeneration. The method is useful for
CC    treating neurological disorders, preferably motorneuron disorders. These
CC    methods can reduce motoneuron loss by 20% or greater in response to nerve
CC    avulsion. This sequence represents cDNA encoding the rat MGF.
XX
SQ    Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

    Query Match              100.0%;  Score 539;  DB 24;  Length 539;
    Best Local Similarity    100.0%;  Pred. No. 1.9e-142;
    Matches  539;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539

RESULT 3
ABV76185
ID    ABV76185 standard; cDNA; 651 BP.
XX
AC    ABV76185;
XX
DT    07-MAR-2003   (first entry)
XX
DE    Mouse insulin-like growth factor IB cDNA.
XX
KW    Insulin-like growth factor IB; IGF-IB; mouse; mRNA; assay;
KW    nucleic acid detection; gene; ss.
XX
OS    Mus musculus.
XX
FH    Key             Location/Qualifiers
FT    CDS             73..474
FT                    /*tag=  a
FT                    /product= "IGF-IB"
XX
PN    WO200297390-A2.
XX
PD    05-DEC-2002.
XX
PF    31-MAY-2002; 2002WO-SE01056.
XX
PR    01-JUN-2001; 2001SE-0001934.
XX
PA    (BIOV-) BIOVITRUM AB.
XX
PI    Parrow V,  Rosengren L;
XX
DR    WPI; 2003-129529/12.
XX
PT    Quantitating a target nucleic acid in a sample comprises immobilizing,
PT    on a solid support, a sample comprising a target nucleic acid, and
PT    detecting and quantitating signals generated from the antisense and
PT    sense probes -
XX
PS    Example 1; Page 16-17; 18pp; English.
XX
CC    The present sequence is that of cDNA encoding murine insulin-like
CC    growth factor 1B (IGF-IB).  The cDNA was used in an example of the
CC    method of the invention to generate probes for determination of
CC    IGF-IB RNA.  The method comprises a quantitative hybridisation
CC    assay for analysis of mRNA in a target nucleic acid (TNA) sample.
CC    It involves: (i) immobilising the TNA sample on a solid support;
CC    (ii) contacting a labelled antisense probe to a first portion of the
CC    TNA, and a labelled sense probe to a second portion of the TNA;
CC    (iii) detecting and quantitating the signals generated from the
CC  / hybridised probes; and (iv) determining the value represented by
CC    the antisense probe signal minus the sense probe signal, the value
CC    being proportional to the amount of mRNA in the TNA sample.  In an
CC    example of the method, a cDNA clone containing 60 nucleotides from
CC    exon 2 and 179 nucleotides from exon 3 of the mouse IGF-IB gene was

CC    cloned into pGEN-4Z vector.  Linearisation of the plasmid with
CC    EcoRI allowed transcription of a 250-nucleotide antisense probe
CC    using T7 polymerase.  Linearisation with HindIII allowed
CC    transcription of a sense probe of similar length using SP6
CC    polymerase (see ABV76186).  The probes were purified and used to
CC    determine IGF-I RNA in mouse hepatocytes and also in rat hepatocytes.
XX
SQ    Sequence 651 BP; 193 A; 185 C; 149 G; 124 T; 0 other;

   Query Match            84.2%;  Score 453.8;  DB 25;  Length 651;
   Best Local Similarity  92.8%;  Pred. No. 2.5e-118;
   Matches  476;  Conservative    0;  Mismatches   37;  Indels   0;  Gaps   0;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db      139 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 198

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |||
Db      199 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 258

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            |||| ||      ||||||||||| |||| || || ||||| ||||||||||||||||||
Db      319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 378

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            ||||||||||||||||||||||| | ||||||||||| |||||||||| ||||||||||||
Db      379 ATGCCCAAGACTCAGAAGTCCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
            |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            |||||||||||||||||||||||| ||| ||||||||||||| |||||||| ||||||||
Db      499 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558

Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            ||||||||||||||||||||||||||| ||||||| |||||||| ||||||| ||| |||||
Db      559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618

Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAA 513
            |||| || |||||||||||||| |||||||||
Db      619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651


RESULT 4
AAD06404
ID    AAD06404 standard; cDNA; 487 BP.
XX
AC    AAD06404;
XX
DT    10-AUG-2001  (first entry)

```
CC   injury that affects motoneurones, motoneurone loss associated with aging,
CC   autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC   peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC   The present sequence is rat liver-type IGF-I isoform (L.IGF-I) cDNA.
CC   The L.IGF-I protein comprises amino acid sequences encoded by
CC   nucleic acid sequence of IGF-I exons 4 and 6.
XX
SQ   Sequence 487 BP; 139 A; 123 C; 126 G; 99 T; 0 other;

  Query Match              78.8%;  Score 425;  DB 22;  Length 487;
  Best Local Similarity    90.4%;  Pred. No. 3.1e-110;
  Matches   487;  Conservative    0;  Mismatches    0;  Indels   52;  Gaps    1;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
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Db        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
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Db       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            |||||||||||||||||||||||||||||||||.||||||||||||||||||||||||||
Db      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            |||||||||||||||||
Db      241 ATGCCCAAGACTCAG--------------------------------------------- 255

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      256 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 308

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      309 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 368

Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      369 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 428

Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      429 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 487


RESULT 5
AAS16883
ID   AAS16883 standard; cDNA; 487 BP.
XX
AC   AAS16883;
XX
DT   25-FEB-2002  (first entry)
```

```
CC    whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC    MGF prevents or diminishes degeneration. The method is useful for
CC    treating neurological disorders, preferably motorneuron disorders. These
CC    methods can reduce motoneuron loss by 20% or greater in response to nerve
CC    avulsion. This sequence represents cDNA encoding the rat insulin-like
CC    growth factor I liver-type isoform (L.IGF-I) used in experiments on
CC    motoneuron loss.
XX
SQ    Sequence 487 BP; 139 A; 123 C; 126 G; 99 T; 0 other;
```

Query Match          78.8%;  Score 425;  DB 24;  Length 487;
Best Local Similarity 90.4%;  Pred. No. 3.1e-110;
Matches  487;  Conservative  0;  Mismatches  0;  Indels  52;  Gaps  1;

```
Qy     · 1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           ||||||||||||||||
Db     241 ATGCCCAAGACTCAG--------------------------------------------- 255

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     256 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 308

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     309 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 368

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     369 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 428

Qy     481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     429 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 487
```

RESULT 6
AAX27498
ID    AAX27498 standard; DNA; 1052 BP.
XX
AC    AAX27498;
XX

CC    This sequence represents the liver isoform of the rat insulin-like
CC    growth factor 1 (IGF1) from rats.  IGF-1 or a modified or biologically
CC    active portion can be used for increasing vertebrate muscle mass by
CC    intramuscular administration, for e.g. (i) preserving or enhancing
CC    muscle strength in aging humans; (ii) healing injured muscle more
CC    efficiently/rapidly; (iii) controlling muscle mass during disease and/or
CC    prolonged stays in reduced gravity; (iv) cosmetic body sculpting; and
CC    (v)  promoting glucose clearance from diabetic muscle tissue.
XX
SQ    Sequence 1052 BP; 301 A; 256 C; 225 G; 270 T; 0 other;

   Query Match              74.7%;  Score 402.6;  DB 20;  Length 1052;
   Best Local Similarity    88.5%;  Pred. No. 8.9e-104;
   Matches  470;  Conservative    0;  Mismatches    9;  Indels   52;  Gaps    1;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      109 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 168


Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      169 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 228


Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      229 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 288

```
Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
          ||||   |      ||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 348

Qy    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
          |||||||||||||||
Db    349 ATGCCCAAGACTCAG--------------------------------------------- 363

Qy    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 416

Qy    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    417 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 476

Qy    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    477 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 536

Qy    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    537 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 587
```

RESULT 7
AAD06400
```
ID    AAD06400 standard; cDNA; 523 BP.
XX
AC    AAD06400;
XX
DT    10-AUG-2001  (first entry)
XX
DE    Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW    Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW    mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW    amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW    poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW    nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW    sex-linked muscular dystrophy; peripheral neuropathy;
KW    Alzheimer's disease; Parkinson's disease; ss.
XX
OS    Oryctolagus cuniculus.
XX
FH    Key             Location/Qualifiers
FT    CDS             1..336
FT                    /*tag=  a
FT                    /product= "Mechano-growth factor (MGF)"
FT                    /note= "This region comprises exons 3-6. The CDS does
FT                    not include start codon"
FT                    /partial
XX
PN    WO200136483-A1.
XX
PD    25-MAY-2001.
XX
```

PT    Use of mechano-growth factor, an isoform of Insulin-like Growth
PT    Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT    medicament for the treatment of neurological disorder -
XX
PS    Claim 4; Page 53-54; 66pp; English.
XX
CC    The present invention relates to use of mechano-growth factor (MGF),
CC    an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC    medicament for the treatment of neurological disorder. The MGF is capable
CC    of reducing motoneurone loss by 20% or greater in response to nerve
CC    avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC    rescue. The MGF polynucleotide and polypeptide are useful in the
CC    manufacture of a medicament for the treatment of a neurological disorder,
CC    including a disorder of motoneurones and/or neurodegenerative disorder,
CC    e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC    spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC    poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC    toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC    injury that affects motoneurones, motoneurone loss associated with aging,
CC    autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC    peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC    The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
CC    isoform having extracellular (Ec) domain, hence also referred as
CC    IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC    nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC    of MGF.
XX
SQ    Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

   Query Match            66.2%;  Score 356.8;  DB 22;  Length 523;
   Best Local Similarity   82.3%;  Pred. No. 6.3e-91;
   Matches   436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||  |||||| || ||||| |||||||||||||| ||||||||||||||||||||||
Db        1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60


Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||| ||||||||||||||||| || ||||||||| ||||||||||||| |||
Db       61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120


Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || |||||| |||||||||| |||||||||||||||||||||||||||||||||||||||
Db      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180


Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

```
            ||||  | .|  |||||||  ||||| |||| || ||| ||||.|||||||||||||| |||
Db      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            |||||||||||||||||| ||||| | ||| ||  |||||||||| |||| || |||
Db      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
            |||||||||||||||||| |||||||||||||||||||||| |||||||||||||| |||
Db      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            ||| |||||||| || ||| | ||||||      | ||| | || | |||||||| || ||||||
Db      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
            ||            |       ||||||| |||| ||| ||||       || ||| |||| ||
Db      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474

Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
            |||||||| |||| |||||||||| ||||||||||||||||||||||||
Db      475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523


RESULT 8
AAS16879
ID    AAS16879 standard; cDNA; 523 BP.
XX
AC    AAS16879;
XX
DT    25-FEB-2002  (first entry)
XX
DE    Rabbit mechano-growth factor (MGF) cDNA.
XX
KW    Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW    neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW    muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW    nerve avulsion.
XX
OS    Oryctolagus cuniculus.
XX
FH    Key             Location/Qualifiers
FT    CDS             1..336
FT                    /*tag=  a
FT                    /product= "Rabbit MGF"
FT                    /partial
FT                    /note= "No start codon"
FT    exon            1..76
FT                    /*tag=  b
FT                    /number= 3
FT    exon            77..259
FT                    /*tag=  c
FT                    /number= 4
FT    exon            260..309
FT                    /*tag=  d
FT                    /number= 5
FT    exon            311..333
```

PT   Use of insulin-like growth factor I (IGF-I) isoform known as
PT   mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT   ability to reduce motoneuron loss in response to nerve avulsion, to
PT   treat nerve damage  -
XX
PS   Disclosure; Fig 7; 65pp; English.
XX
CC   The invention relates to the use of an insulin-like growth factor I
CC   (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC   of a medicament for treating nerve damage in the peripheral nervous
CC   system, or for treating nerve damage by localising MGF at the site of
CC   damage. The nerve damage may include severing of a nerve. The treatment
CC   may be combined with another treatment (such as a polypeptide growth
CC   factor other than MGF) that prevents or diminishes degeneration of the
CC   target organ (for example, muscle) which the damaged nerve innervates,
CC   whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC   MGF prevents or diminishes degeneration. The method is useful for
CC   treating neurological disorders, preferably motorneuron disorders. These
CC   methods can reduce motoneuron loss by 20% or greater in response to nerve
CC   avulsion. This sequence represents cDNA encoding the rabbit MGF.
XX
SQ   Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

  Query Match              66.2%;   Score 356.8;   DB 24;   Length 523;
  Best Local Similarity    82.3%;   Pred. No. 6.3e-91;
  Matches   436;  Conservative    0;  Mismatches    87;  Indels    7;  Gaps    2;

```
Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||| |||||| || ||||| ||||||||||||| ||||||||||||||||||||||||
Db        1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||| |||||||||||||||| || ||||||||| |||||||||| |||
Db       61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || |||||| |||||||||| |||||||||||||||||||||||||||||||||||||||
Db      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
```

```
Qy    181  TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
                |||| | |  ||||||| ||||| |||| || ||| |||| |||||||||||||||| |||
Db    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241  ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
                |||||||||||||||||||| ||||| | ||| || ||||||||| |||| || |||
Db    241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy    301  AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                |||||||||||||||||| ||||||||||||||||||||| ||||||||||||||| |||
Db    301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy    361  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
                ||| ||||||||| || ||| | |||||    | ||| | || | |||||||| || ||||||
Db    361  CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy    421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
                || |        | |||||| |||| ||| |||| ||        || ||| |||| ||
Db    421  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474

Qy    481  TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
                |||||||| ||||| ||||||||||| ||||||||||||||||||||||||
Db    475  ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
```

RESULT 9
AAT84893
ID    AAT84893 standard; cDNA; 553 BP.
XX
AC    AAT84893;
XX
DT    14-APR-1998   (first entry)
XX
DE    Rabbit insulin like growth factor 1 encoding cDNA.
XX
KW    Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;
KW    heart; neuromuscular disease; primer; ss.
XX
OS    Oryctolagus cuniculus.
XX
FH    Key             Location/Qualifiers
FT    CDS             1..366
FT                    /*tag=   a
FT                    /product= "IGF-1"
XX
PN    WO9733997-A1.
XX
PD    18-SEP-1997.
XX
PF    11-MAR-1997;    97WO-GB00658.
XX
PR    11-MAR-1996;    96GB-0005124.
XX
PA    (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI    Goldspink G;

```
   Query Match              66.2%;  Score 356.8;  DB 18;  Length 553;
   Best Local Similarity    82.3%;  Pred. No. 6.4e-91;
   Matches   436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           ||||| |||||| || |||||| ||||||||||||||| ||||||||||||||||||||||
Db      31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           |||||||||| |||||||||||||| || |||||||||| ||||||||||||| |||
Db      91 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           || |||||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           |||| | | |||||| ||||| |||| || ||| |||| |||||||||||||| |||
Db     211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           ||||||||||||||||||||| ||||| | ||| || |||||||||| |||| || | |||
Db     271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
           |||||||||||||||||| ||||||||||||||||||||| ||||||||||||||||| |||
Db     331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||| |||||||| || ||| | |||||     | || | || | |||||| || ||||||
Db     391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450
```

```
Qy    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
          ||          |    |||||| |||| ||| ||||      || ||| |||| ||
Db    451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 504

Qy    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
          ||||||| |||| |||||||||| ||||||||||||||||||||||||||
Db    505 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553
```

RESULT 10
AAD06398
ID    AAD06398 standard; cDNA; 517 BP.
XX
AC    AAD06398;
XX
DT    10-AUG-2001  (first entry)
XX
DE    Human IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW    Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW    mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW    amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW    poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW    nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW    sex-linked muscular dystrophy; peripheral neuropathy;
KW    Alzheimer's disease; Parkinson's disease; ss.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    CDS             1..333
FT                    /*tag=  a
FT                    /product= "Mechano-growth factor (MGF)"
FT                    /note= "This region comprises exons 3-6. The CDS does
FT                    not include start codon"
FT                    /partial
XX
PN    WO200136483-A1.
XX
PD    25-MAY-2001.
XX
PF    15-NOV-2000; 2000WO-GB04354.
XX
PR    15-NOV-1999;   99GB-0026968.
XX
PA    (UNLO ) UNIV COLLEGE LONDON.
XX
PI    Goldspink G,  Johnson I;
XX
DR    WPI; 2001-355620/37.
DR    P-PSDB; AAE02447.
XX
PT    Use of mechano-growth factor, an isoform of Insulin-like Growth
PT    Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT    medicament for the treatment of neurological disorder -
XX
```

PS    Claim 4; Page 49-50; 66pp; English.
XX
CC    .The present invention relates to use of mechano-growth factor (MGF),
CC    an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC    medicament for the treatment of neurological disorder. The MGF is capable
CC    of reducing motoneurone loss by 20% or greater in response to nerve
CC    avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC    rescue. The MGF polynucleotide and polypeptide are useful in the
CC    manufacture of a medicament for the treatment of a neurological disorder,
CC    including a disorder of motoneurones and/or neurodegenerative disorder,
CC    e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC    spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC    poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC    toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC    injury that affects motoneurones, motoneurone loss associated with aging,
CC    autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC    peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC    The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
CC    isoform having extracellular (Ec) domain, hence also referred as
CC    IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC    nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC·   of MGF.
XX
SQ    Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

   Query Match              60.3%;   Score 325.2;   DB 22;   Length 517;
   Best Local Similarity    81.2%;   Pred. No. 5.4e-82;
   Matches   429;   Conservative     0;   Mismatches    88;   Indels   11;   Gaps    4;

```
Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||  ||||||  ||  ||||||||||||||||||||||| ||||||||||||||||||
Db        1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||| ||||||||||||||| |||||||||||| ||||||||| || |||
Db       61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            .|| |||||| ||||||||||| ||||||||||||||||||||| |||||||||||||||
Db      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            || |  || |||||||| | |||||||||||| || |||| |||||||||||||||| |||
Db      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            |||||||||| |||||||  ||||||| ||| || ||||||| | |||| || |
Db      241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
            ||||||||||||||||||| ||||||||||||||||||||| ||||||||||||||| |||
Db      298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            ||| ||||||| || || ||| | ||||||    | || | || | |||||||| || ||||||
Db      358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
```

```
Qy      421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
             ||          |       |||||| |||| ||| ||||       || ||| |||| ||
Db      417  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAATAAGTTTGATC 470

Qy      481  TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACAT 528
             ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db      471  ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
```

RESULT 11
AAS16877
ID   AAS16877 standard; cDNA; 517 BP.
XX
AC   AAS16877;
XX
DT   25-FEB-2002   (first entry)
XX
DE   Human mechano-growth factor (MGF) cDNA.
XX
KW   Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW   neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW   nerve avulsion.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..333
FT                   /*tag=  a
FT                   /product= "Human MGF"
FT                   /partial
FT                   /note= "No start codon"
FT   exon            1..76
FT                   /*tag=  b
FT                   /number= 3
FT   exon            77..259
FT                   /*tag=  c
FT                   /number= 4
FT   exon            260..307
FT                   /*tag=  d
FT                   /number= 5
FT   exon            308..330
FT                   /*tag=  e
FT                   /number= 6
XX
PN   WO200185781-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-GB02054.
XX
PR   10-MAY-2000; 2000GB-0011278.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
PA   (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI   Goldspink G,  Terenghi G;
```

```
XX
DR    WPI; 2002-055585/07.
DR    P-PSDB; AAU10559.
XX
PT    Use of insulin-like growth factor I (IGF-I) isoform known as
PT    mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT    ability to reduce motoneuron loss in response to nerve avulsion, to
PT    treat nerve damage  -
XX
PS    Claim 11; Fig 5; 65pp; English.
XX
CC    The invention relates to the use of an insulin-like growth factor I
CC    (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC    of a medicament for treating nerve damage in the peripheral nervous
CC    system, or for treating nerve damage by localising MGF at the site of
CC    damage. The nerve damage may include severing of a nerve. The treatment
CC    may be combined with another treatment (such as a polypeptide growth
CC    factor other than MGF) that prevents or diminishes degeneration of the
CC    target organ (for example, muscle) which the damaged nerve innervates,
CC    whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC    MGF prevents or diminishes degeneration. The method is useful for
CC    treating neurological disorders, preferably motorneuron disorders. These
CC    methods can reduce motoneuron loss by 20% or greater in response to nerve
CC    avulsion. This sequence represents cDNA encoding the human MGF.
XX
SQ    Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;
```

```
   Query Match            60.3%;   Score 325.2;   DB 24;   Length 517;
   Best Local Similarity  81.2%;   Pred. No. 5.4e-82;
   Matches   429;  Conservative    0;  Mismatches    88;  Indels    11;  Gaps    4;
```

```
Qy         1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
             ||||| ||||| || ||||||||||||||||||||||| ||||||||||||||||||||||
Db         1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60


Qy        61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
             |||||||||||| |||||||||||||||||| ||||||||||||| ||||||||| | |||
Db        61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120


Qy       121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
             || ||||| ||||||||||| ||||||||||||||||||||| |||||||||||||||||
Db       121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180


Qy       181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
             || |  || ||||||| | |||||||||| ||  |||| ||||||||||||||| |||
Db       181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240


Qy       241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
             |||||||||| ||||||| ||||||| ||| || ||||||| | |||| || | 
Db       241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297


Qy       301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
             |||||||||||||||||| ||||||||||||||||||| |||||||||||||||||| |||
Db       298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357


Qy       361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
             ||| |||||| || || ||| | |||||    | || | || | |||||||| || ||||||
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```
Db       358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy       421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
             ||           |    |||||| |||| ||| ||||     || ||| |||| ||
Db       417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 470

Qy       481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACAT 528
             ||||||| |||| |||||||||||| |||||||||||||||||||||||
Db       471 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
```

RESULT 12
ABT09479
ID     ABT09479 standard; DNA; 671 BP.
XX
AC     ABT09479;
XX
DT     05-DEC-2002   (first entry)
XX
DE     Phase-1 Rat CT gene SEQ ID No 567.
XX
KW     Rat; toxicity study; rat toxic response gene; toxicological response;
KW     drug development; phase-1 rat CT gene; ds.
XX
OS     Rattus sp.
XX
PN     WO200266682-A2.
XX
PD     29-AUG-2002.
XX
PF     29-JAN-2002; 2002WO-US02935.
XX
PR     29-JAN-2001; 2001US-264933P.
PR     26-JUL-2001; 2001US-308161P.
XX
PA     (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI     Farris G,  Hicken SH,  Farr SB;
XX
DR     WPI; 2002-674961/72.
XX
PT     Evaluating the toxicity of an agent, useful in drug development or in
PT     determining toxicological responses to a new drug, by determining the
PT     expression of rat toxicologically relevant genes in the test animal in
PT     response to the test agent  -
XX
PS     Disclosure; Page 245; 388pp; English.
XX
CC     The invention relates to a method used for evaluating the toxicity of an
CC     agent comprising determining the expression of a rat toxic response
CC     gene(s) in the test animal in response to the agent. The method is useful
CC     in drug development, particularly for conducting toxicity studies and
CC     analysis before a new drug or compound is approved for human consumption
CC     or use. The method is also useful in determining toxicological responses
CC     to a new drug. This polynucleotide sequence represents a phase-1 rat CT
CC     gene of the invention.
XX
```

SQ    Sequence 671 BP; 160 A; 181 C; 180 G; 150 T; 0 other;

  Query Match                 55.6%;   Score 299.6;   DB 24;   Length 671;
  Best Local Similarity       97.1%;   Pred. No. 1e-74;
  Matches  305;  Conservative     0;  Mismatches     9;  Indels     0;  Gaps     0;

```
Qy         1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       140 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAATTCGTGTGTGGACCA 199

Qy        61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       200 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 259

Qy       121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       260 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 319

Qy       181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
             |||| |      |||||||||||||||||||||||||||||||||||||||||||||||||
Db       320 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 379

Qy       241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       380 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 439

Qy       301 AGAAGGAAAGGAAG 314
             ||||||||||||||
Db       440 AGAAGGAAAGGAAG 453
```

RESULT 13
AAN70436
ID    AAN70436 standard; cDNA; 818 BP.
XX
AC    AAN70436;
XX
DT    25-MAR-2003   (updated)
DT    05-APR-1991   (first entry)
XX
DE    Sequence encoding insulin-like growth factor 1A (IGF-1A).
XX
KW    Growth promoter; lactation enhancer;  cell proliferation; ss.
XX
OS    Homo sapiens.
XX
PN    EP229750-A.
XX
PD    22-JUL-1987.
XX
PF    06-JAN-1987;    87EP-0870001.
XX
PR    20-NOV-1986;    86US-0929671.
PR    07-JAN-1986;    86US-0816662.
XX
PA    (UNIW ) UNIV WASHINGTON.
XX

```
  Query Match                50.9%;  Score 274.2;  DB 8;  Length 818;
  Best Local Similarity   76.0%;  Pred. No. 1.7e-67;
  Matches  405;  Conservative   0;  Mismatches   68;  Indels   60;  Gaps    3;


Qy         1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
             ||||| |||||| || ||||||||||||||||||||||| |||||||||||||||||||||
Db       203 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 262


Qy        61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
             |||||||||| ||||||||||||||| |||||||||||| |||||||| || |||
Db       263 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 322


Qy       121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
             || |||||| ||||||||||| |||||||||||||||||||| |||||||||||||||||
Db       323 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 382


Qy       181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
             || |   || | |||||||| | |||||||||| || |||| |||||||||||||| |||
Db       383 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 442


Qy       241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
             |||||||||||| |||
Db       443 ATGCCCAAGACCCAG--------------------------------------------- 457


Qy       301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                   ||||||||||| ||||||||| ||||||||| |||||||||||||||||| |||
Db       458 ------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 510


Qy       361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
             ||| ||||||||| || ||||| |||||    |  || || | |||||||| ||||||||
Db       511 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 570


Qy       421 --CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAA 478
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           ||||   |||  |||||  |||| | ||||||||| |||       || ||| |||| |
Db     571 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCA------AAAAATAAGTTTGA 624

Qy     479 TATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
           || |||||| | ||||||||| |||||| ||||||||||||||||||||||||||
Db     625 TAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTCC 677
```

RESULT 14
ABT11091
ID     ABT11091 standard; cDNA; 7260 BP.
XX
AC     ABT11091;
XX
DT     04-DEC-2002   (first entry)
XX
DE     Human breast cancer associated coding sequence SEQ ID NO: 1225.
XX
KW     Human; breast specific gene; breast cancer; differential expression;
KW     cytostatic; gene therapy; gene; ss.
XX
OS     Homo sapiens.
XX
PN     WO200259271-A2.
XX
PD     01-AUG-2002.
XX
PF     25-JAN-2002; 2002WO-US02176.
XX
PR     25-JAN-2001; 2001US-263757P.
PR     25-APR-2001; 2001US-286090P.
PR     23-MAY-2001; 2001US-292517P.
XX
PA     (GENE-) GENE LOGIC INC.
XX
PI     Orr MS,  Nation M,  Diggans JC,  Zeng W;
XX
DR     WPI; 2002-674803/72.
XX
PT     Diagnosing breast cancer in a patient comprises detecting the level of
PT     gene expression in cell or tissue samples, where a differential gene
PT     expression is indicative of breast cancer  -
XX
PS     Claim 1; SEQ ID NO 1225; 260pp + Sequence Listing; English.
XX
CC     The present invention relates to methods of diagnosing breast cancer in a
CC     patient, which comprise detecting the level of expression in a tissue
CC     sample of two or more genes selected from those shown in ABT09867-
CC     ABT11112, where a differential expression of the genes indicates breast
CC     cancer. The methods are useful in diagnosing, treating, detecting the
CC     progression, and in monitoring treatment of breast cancer in patients.
CC     The methods are also useful as a screening tool for agents that modulate
CC     the onset or progression of breast cancer. The breast cancer genes may be
CC     used as diagnostic markers for the prediction or identification of the
CC     malignant state of breast tissue, for confirming the type and progression
CC     of cancer, and for drug screening and assays. The present sequence is a
CC     coding sequence of the invention.
```

XX
SQ   Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

  Query Match            50.9%;  Score 274.2;  DB 24;  Length 7260;
  Best Local Similarity  76.0%;  Pred. No. 3.6e-67;
  Matches  405;  Conservative   0;  Mismatches  68;  Indels  60;  Gaps   3;

Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           |||||  ||||||  ||  ||||||||||||||||||||||  ||||||||||||||||||||||
Db     311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           ||||||||||| ||||||||||||||||||| ||||||||||||| |||||||| || |||
Db     371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           || |||||  ||||||||||||  |||||||||||||||||| ||||||||||||||||||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           ||| |   ||   ||||||| | |||||||||||  | |||| ||||||||||||||| |||
Db     491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           ||||||||||||| |||
Db     551 ATGCCCAAGACCCAG--------------------------------------------- 565

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                  |||||||||||  ||||||||| |||||||||| |||||||||||||||||||  |||
Db     566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||| ||||||||| || |||||| |||||    | | || || | |||||||| |||||||||
Db     619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 --CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAA 478
             ||||   |||  |||||  ||||  | ||||||||| |||        || ||| |||| |
Db     679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCA------AAAAATAAGTTTGA 732

Qy     479 TATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
           || |||||| | |||||||| ||||||| ||||||||||||||||||||||||||||||
Db     733 TAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTCC 785


RESULT 15
ABK84583
ID   ABK84583 standard; cDNA; 7260 BP.
XX
AC   ABK84583;
XX
DT   14-AUG-2002   (first entry)
XX
DE   Human cDNA differentially expressed in granulocytic cells #1154.
XX

CC    The invention relates to detecting (M1) granulocyte (GC) activation
CC    (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC    DNA chip analysis as given in the specification, and comparing
CC    the expression level to an expression level in an unactivated
CC    GC, where differential expression of Gs is indicative of GCA.
CC    Also included are modulating (M2) GA by contacting GC with an agent
CC    that alters the expression of at least one gene in Gs; (2) screening (M3)
CC    for an agent capable of modulating GCA or an inflammation (especially
CC    chronic) in a tissue, an allergic response in a subject, exposure of a
CC    subject to a pathogen or sterile inflammatory disease using the
CC    gene expression profile; (3) detecting (M4) an inflammation (especially
CC    chronic) in a tissue, an allergic response in a subject, exposure of a
CC    subject to a pathogen or sterile inflammatory disease, by detecting the
CC    level of expression in a sample of the tissue of gene(s) from Gs, where
CC    the level of expression of the gene is indicative of inflammation;
CC    (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC    an allergic response in a subject, exposure of a subject to a pathogen
CC    or sterile inflammatory disease, by contacting a tissue having
CC    inflammation with an agent that modulates the expression of gene(s)
CC    from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC    modulating GA; M3 is useful for screening an agent capable of modulating
CC    GCA preferably in an inflammation in a tissue; M4 is useful for
CC    detecting an inflammation (especially chronic) in a tissue, an allergic
CC    response in a subject, exposure of a subject to a pathogen or sterile
CC    inflammatory disease (e.g. psoriasis, rheumatoid arthritis,

CC   glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC   reperfusion injury, ARDS, adult respiratory distress syndrome,
CC   inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC   periodontal disease; also bacterial infection, viral infection,
CC   parasitic infection, protozoal infection, fungal infection and M5 is
CC   useful for treating one of the above conditions. The present
CC   sequence represents a gene differentially expressed in granulocytes.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

    Query Match          50.9%;  Score 274.2;  DB 24;  Length 7260;
    Best Local Similarity  76.0%;  Pred. No. 3.6e-67;
    Matches  405;  Conservative    0;  Mismatches   68;  Indels   60;  Gaps    3;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||  ||||||  ||  ||||||||||||||||||||||||  ||||||||||||||||||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||||  ||||||||||||||||||||||  |||||||||||||  ||||||||||  ||  |||
Db      371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            ||  |||||  |||||||||||  |||||||||||||||||||||||  ||||||||||||||||||
Db      431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            ||  |    ||  |||||||| |  ||||||||||||  ||    ||||  |||||||||||||||  |||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            ||||||||||||  |||
Db      551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                   ||||||||||  |||||||||  |||||||||  ||||||||||||||||||||||  |||
Db      566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            |||  ||||||||||  ||  |||||  |||||      |  ||  ||  |  |||||||||  |||||||||||
Db      619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy      421 --CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAA 478
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Qy      479 TATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
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Db      733 TAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTCC 785


Search completed: December 13, 2003, 06:03:49
Job time : 217.419 secs

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                         GenCore version 5.1.6
                Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          December 13, 2003, 06:03:55 ; Search time 49.8379 Seconds
                                            (without alignments)
                                            4773.589 Million cell updates/sec


Title:           US-09-852-261-3
Perfect score:   539
Sequence:.       1 ggaccagagaccctttgcgg..........agtaaacattcccggaattc 539


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


Searched:        569978 seqs, 220691566 residues


Total number of hits satisfying chosen parameters:      1139956


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
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                 Listing first 45 summaries


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         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.


                                  SUMMARIES
                        %
Result              Query
   No.    Score  Match Length DB  ID                        Description
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      1   356.8   66.2    553  3  US-09-142-583A-3          Sequence 3, Appli
      2   356..8  66.2    553  3  US-09-142-583A-5          Sequence 5, Appli
      3   272.6   50.6    777  3  US-09-142-583A-10         Sequence 10, Appl
      4   271     50.3    622  6  5405942-2                 Patent No. 5405942
      5   222     41.2   5707  2  US-08-472-809B-8          Sequence 8, Appli
      6   222     41.2   6345  2  US-08-472-809B-7          Sequence 7, Appli
      7   205.2   38.1    357  6  5405942-9                 Patent No. 5405942
      8   203.6   37.8    357  6  5405942-13                Patent No. 5405942
      9   166.8   30.9    210  6  5405942-7                 Patent No. 5405942
     10   166.8   30.9    210  6  5405942-11                Patent No. 5405942
     11   166.8   30.9   2862  4  US-09-255-829-13          Sequence 13, Appl
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         12   165.2   30.6    210   6   5405942-15           Patent No. 5405942
         13   161.2   29.9    240   1   US-08-308-196A-1      Sequence 1, Appli
         14   161.2   29.9    240   5   PCT-US91-06452-1      Sequence 1, Appli
         15   161.2   29.9    390   3   US-09-029-267-13      Sequence 13, Appl
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         17    146    27.1    770   1   US-07-953-230A-1      Sequence 1, Appli
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         23   109.8   20.4    485   1   US-07-989-845-29      Sequence 29, Appl
         24   109.8   20.4    485   1   US-07-989-844-13      Sequence 13, Appl
         25   109.8   20.4    485   1   US-08-110-663-1       Sequence 1, Appli
         26   109.8   20.4    485   1   US-08-169-688-1       Sequence 1, Appli
         27   109.8   20.4    485   1   US-08-240-121-13      Sequence 13, Appl
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         31   109.8   20.4    485   1   US-08-385-187A-1      Sequence 1, Appli
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         33   109.8   20.4    485   5   PCT-US93-11297-13     Sequence 13, Appl
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         37   107.6   20.0    717   1   US-08-284-784-40      Sequence 40, Appl
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         40   107.6   20.0    783   2   US-08-854-811-43      Sequence 43, Appl
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         42   107.6   20.0    891   1   US-08-284-784-34      Sequence 34, Appl
         43   107.6   20.0    891   2   US-08-854-811-33      Sequence 33, Appl
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         45   107.6   20.0    900   1   US-08-284-784-24      Sequence 24, Appl
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ALIGNMENTS


RESULT 1
US-09-142-583A-3
; Sequence 3, Application US/09142583A
; Patent No. 6221842
;    GENERAL INFORMATION:
;         APPLICANT: GOLDSPINK, GEOFFREY
;         TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
;         NUMBER OF SEQUENCES: 11
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: NIXON & VANDERHYE P.C.
;              STREET: 1100 NORTH GLEBE ROAD
;              CITY: ARLINGTON
;              STATE: VA
;              COUNTRY: USA
;              ZIP: 22201
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible

  Query Match              66.2%;   Score 356.8;   DB 3;    Length 553;
  Best Local Similarity    82.3%;   Pred. No. 2.5e-109;
  Matches  436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
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Db     31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
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Db     91 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
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Db    211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
          |||||||||||||||||||| ||||| | ||| || ||||||||| |||| || |||
Db    271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
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Db     331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||| ||||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db     391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
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Db     505 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553
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RESULT 2
US-09-142-583A-5
; Sequence 5, Application US/09142583A
; Patent No. 6221842
;   GENERAL INFORMATION:
;       APPLICANT: GOLDSPINK, GEOFFREY
;       TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
;       NUMBER OF SEQUENCES: 11
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: NIXON & VANDERHYE P.C.
;           STREET: 1100 NORTH GLEBE ROAD
;           CITY: ARLINGTON
;           STATE: VA
;           COUNTRY: USA
;           ZIP: 22201
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/142,583A
;           FILING DATE: 29-Oct-1998
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: WO PCT/GB97/00658
;           FILING DATE: 11-MAR-1997
;           APPLICATION NUMBER: GB 9605124.8
;           FILING DATE: 11-MAR-1996
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SADOFF, B. J.
;           REGISTRATION NUMBER: 36663
;           REFERENCE/DOCKET NUMBER: 117-263
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 7038164000
;           TELEFAX: 7038164100
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 553 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: both
;           TOPOLOGY: linear

  Query Match            66.2%;  Score 356.8;  DB 3;   Length 553;
  Best Local Similarity  82.3%;  Pred. No. 2.5e-109;
  Matches  436;  Conservative   0;  Mismatches   87;  Indels   7;  Gaps   2;

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Db      31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
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Db      91 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db     151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           ||||.|.|.|||||||.|||||.||||.|||.||.|||.||||.||||||||||||.|||
Db     211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
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Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
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Db     331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
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Db     391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
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Db     505 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553
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RESULT 3
US-09-142-583A-10
; Sequence 10, Application US/09142583A
; Patent No. 6221842
;    GENERAL INFORMATION:
;        APPLICANT: GOLDSPINK, GEOFFREY
;        TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:

;  INFORMATION FOR SEQ ID NO: 10:
;     SEQUENCE CHARACTERISTICS:
;          LENGTH: 777 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: both
;          TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     FEATURE:
;          NAME/KEY: CDS
;          LOCATION: 26..493
;     SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-142-583A-10

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   Best Local Similarity   75.8%;   Pred. No. 4.3e-81;
   Matches  404;  Conservative    0;  Mismatches   69;  Indels   60;  Gaps    3;

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Db      179 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 238

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
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Db      239 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 298

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || || || |||||||||||||  ||||||||||||||||||||  |||||||||||||||
Db      299 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 358

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

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Qy     241  ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
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Db     419  ATGCCCAAGACCCAG--------------------------------------------- 433

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Db     434  -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 486

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RESULT 4
5405942-2
;Patent No. 5405942
;    APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;    NUMBER OF SEQUENCES: 16
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/65,673
;      FILING DATE: 16-JUN-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 630,557
;      FILING DATE: 19-JUL-1984
;SEQ ID NO:2:
;      LENGTH: 622
5405942-2

  Query Match            50.3%;  Score 271;  DB 6;  Length 622;
  Best Local Similarity  61.2%;  Pred. No. 1.3e-80;
  Matches  326;  Conservative   77;  Mismatches   70;  Indels   60;  Gaps    3;

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Db      45  GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 104

Qy      61  AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||:::::| ::||||||||||||||||| :|:|||:||||||| :|||||||| || |||
Db     105  AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 164

Qy     121  ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || || |: |:|||:|||:| :||::||||||||:|:||:| |||||||:|||||:|:|
Db     165  ACAGGUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCAUAGGAGGCUGGAGAUGUAU 224
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Qy        181  TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
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Db        225  UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGCUCUGUCCGUGCCCAGCGCCACACCGAC 284


Qy        241  ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
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Db        285  AUGCCCAAGACCCAG--------------------------------------------- 299


Qy        301  AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
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Db        300  -------AAGGAAGUACAUUUGAAGAACGCAAGUAGAGGGAGUGCAGGAAACAAGAACUA 352


Qy        361  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
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Qy        421  --CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAA 478
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Db        413  CUCUGCACGAGUUACCUGUUAAACUUUGGAACACCUACCA------AAAAAUAAGUUUGA 466


Qy        479  TATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
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Db        467  UAACAUUUAAAAGAUGGGCGUUUCCCCCAAUGAAAUACACAAGUAAACAUUCC 519
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RESULT 5
US-08-472-809B-8
; Sequence 8, Application US/08472809B
; Patent No. 5925564
;  GENERAL INFORMATION:
;    APPLICANT:  Schwartz, Robert J.
;    APPLICANT:  DeMayo, Franco J.
;    APPLICANT:  O'Malley, Bert W.
;    TITLE OF INVENTION:  Expression Vector Systems and
;    TITLE OF INVENTION:  Method of Use
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,809B
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/209,846
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  Query Match            41.2%;  Score 222;  DB 2;  Length 5707;
  Best Local Similarity  75.5%;  Pred. No. 1.1e-63;
  Matches  314;  Conservative   0;  Mismatches  50;  Indels  52;  Gaps   1;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||  |||||  ||  |||||||||||||||||||||||  |||||||||||||||||||
Db      793 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 852

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||||  |||||||||||||||||   ||||||||||||  ||||||||| || |||
Db      853 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 912

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            ||  |||||  ||||||||||  |||||||||||||||||||||  |||||||||||||||||
Db      913 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 972

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            ||  |  ||  |||||||| |  ||||||||||  ||  |||| ||||||||||||| |||
Db      973 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 1032

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            ||||||||||| ||||
Db     1033 ATGCCCAAGACCCAG--------------------------------------------- 1047

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                   ||||||||||| |||||||| ||||||||||| ||||||||||||||||| |||
Db     1048 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 1100

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCC 416
            ||| |||||||| || |||||| |||||    | || || | |||||||| |||||
Db     1101 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCC 1156


RESULT 6
US-08-472-809B-7
; Sequence 7, Application US/08472809B
; Patent No. 5925564

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Query Match            41.2%;  Score 222;  DB 2;  Length 6345;
Best Local Similarity  75.5%;  Pred. No. 1.2e-63;
Matches  314;  Conservative    0;  Mismatches   50;  Indels   52;  Gaps    1;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||  |||||| ||  ||||||||||||||||||||||| |||||||||||||||||||
Db     3702 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 3761

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||| ||||||||||||||||  |||||||||||| |||||||| || |||
```

```
Db    3762 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 3821

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
               || |||||| ||||||||||| ||||||||||||||||||| ||||||||||||||||||
Db    3822 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 3881

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
               || |  || |  ||||||| | |||||||||| ||  |||| |||||||||||||| |||
Db    3882 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 3941

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
               ||||||||||| |||
Db    3942 ATGCCCAAGACCCAG---------------------------------------------- 3956

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                     ||||||||||| |||||||||| |||||||||| ||||||||||||||||| |||
Db    3957 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 4009

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCC 416
               ||| ||||||||| || ||||| |||||      | | || || | |||||||| |||||
Db    4010 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCC 4065


RESULT 7
5405942-9
;Patent No. 5405942
;     APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;     TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;     NUMBER OF SEQUENCES: 16
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/65,673
;       FILING DATE: 16-JUN-1987
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 630,557
;       FILING DATE: 19-JUL-1984
;SEQ ID NO:9:
;       LENGTH: 357
5405942-9

  Query Match            38.1%;  Score 205.2;  DB 6;  Length 357;
  Best Local Similarity  70.2%;  Pred. No. 9e-59;
  Matches  181;  Conservative    44;  Mismatches    33;  Indels    0;  Gaps    0;

Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
               ||||| |||||| |: :|||||||:||||:||:|||||||:::|||::||:|:|:|||
Db      43 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGACGCUCUUCAGUUCGUGUGUGGAGAC 102

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
               ||||||:::::| ::|||||||||||||||  :|:|||:||||| :|||||||| || |||
Db     103 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 162

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
               || || |: |:|||:|||:| :| ::|||||||||:|:||:|: ||||||:|||||:|:|
Db     163 ACAGGUAUCGUGGAUGAGUGCUGUUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 222
```

```
Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
                :|   |   | |   ||||||: |  |||:||||:|| :|   :||| |||||||||||||||| |||
Db      223 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGCUCUGUCCGUGCCCAGCGCCACACCGAC 282

Qy      241 ATGCCCAAGACTCAGAAG 258
                |:|||||||||| ||||||
Db      283 AUGCCCAAGACCCAGAAG 300
```

RESULT 8
5405942-13
;Patent No. 5405942
;     APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;     TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;     NUMBER OF SEQUENCES: 16
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/07/65,673
;       FILING DATE: 16-JUN-1987
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 630,557
;       FILING DATE: 19-JUL-1984
;SEQ ID NO:13:
;     LENGTH: 357
5405942-13

   Query Match              37.8%;  Score 203.6;  DB 6;  Length 357;
   Best Local Similarity    86.8%;  Pred. No. 3.1e-58;
   Matches  224;  Conservative    0;  Mismatches   34;  Indels   0;  Gaps   0;

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Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
                |||||  |||||| ||  ||||||||||||||||||||||||| ||||||||||||||||||||||
Db       43 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 102

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
                |||||||||||| |||||||||||||||||   ||||||||||||||| |||||||||| || |||
Db      103 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 162

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
                || || ||  ||||||||||| |||||||||||||||||||||| ||||||||||||||||||||
Db      163 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 222

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
                || |   | |   || |||| | ||||||||||| || |||| |||||||||||||| |||
Db      223 TGCGCACCCCTCAGGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 282

Qy      241 ATGCCCAAGACTCAGAAG 258
                |||||||||||| ||||||
Db      283 ATGCCCAAGACCCAGAAG 300
```

RESULT 9
5405942-7
;Patent No. 5405942
;     APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.

```
   Query Match              30.9%;  Score 166.8;  DB 6;   Length 210;
   Best Local Similarity    67.6%;  Pred. No. 4.5e-46;
   Matches  142;  Conservative    41;  Mismatches   27;  Indels   0;  Gaps    0;


Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||| |||||| |: :||||||||:||||:||:||| ||:|::|||::||:|:|:|||
Db        1 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60


Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||:::::|  ::|||||||||||||||||   :|:|||:||||||  :|||||||| || |||
Db       61 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 120


Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || || |: |:|||:|||:|  :||::||||||||:|:||:|:  |||||||:|||||:|:|
Db      121 ACAGGUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180


Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCT 210
            :| |  || |||||: | |||:||||:
Db      181 UGCGCACCCCUCAAGCCUGCCAAGUCAGCU 210
```

```
   Query Match              30.9%;  Score 166.8;  DB 6;   Length 210;
   Best Local Similarity    87.1%;  Pred. No. 4.5e-46;
   Matches  183;  Conservative    0;  Mismatches   27;  Indels   0;  Gaps    0;


Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
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```
          |||||  |||||  ||  ||||||||||||||||||||  |||||||||||||||||||||||||
Db      1  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC  60

Qy     61  AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG  120
           |||||||||||  ||||||||||||||||  |||||||||||||  |||||||||  ||  |||
Db     61  AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG  120

Qy    121  ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC  180
           ||  ||  ||  |||||||||||  ||||||||||||||||||||||  ||||||||||||||||||
Db    121  ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT  180

Qy    181  TGTGTCCGCTGCAAGCCTACAAAGTCAGCT  210
           ||| |   | |  ||||||||  |  ||||||||||||
Db    181  TGCGCACCCCTCAAGCCTGCCAAGTCAGCT  210


RESULT 11
US-09-255-829-13
; Sequence 13, Application US/09255829
; Patent No. 6461617
;  GENERAL INFORMATION:
;     APPLICANT:  Shone, Clifford Charles
;     APPLICANT:  Quinn, Conrad Padraig
;     APPLICANT:  Foster, Keith Alan
;     TITLE OF INVENTION:  Recombinant Toxin Fragments
;     NUMBER OF SEQUENCES:  29
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
;        STREET:  1100 NEW YORK AVENUE, NW, SUITE 600
;        CITY:  WASHINGTON
;        STATE:  DC
;        COUNTRY:  USA
;        ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE:  Floppy disk
;        COMPUTER:  IBM PC compatible
;        OPERATING SYSTEM:  PC-DOS/MS-DOS
;        SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/09/255,829
;        FILING DATE:  23-FEB-1999
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  PCT/GB97/02273
;        FILING DATE:  22-AUG-1997
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US 08/782,893
;        FILING DATE:  27-DEC-1996
;     ATTORNEY/AGENT INFORMATION:
;        NAME:  ESMOND, ROBERT W.
;        REGISTRATION NUMBER:  32,893
;        REFERENCE/DOCKET NUMBER:  1581.0130002
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  202-371-2600
;        TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  2862 base pairs
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   Query Match            30.9%;  Score 166.8;  DB 4;  Length 2862;
   Best Local Similarity  87.1%;  Pred. No. 2.1e-45;
   Matches  183;  Conservative   0;  Mismatches  27;  Indels   0;  Gaps   0;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||  ||||||  ||  ||||||||||||||||||||||  ||||||||||||||||||||
Db     2644 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 2703

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||||  |||||||||||||||||  ||||||||||||||  ||||||||| ||  |||
Db     2704 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 2763

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            ||  ||  ||  |||||||||||  ||||||||||||||||||||  ||||||||||||||||
Db     2764 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 2823

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCT 210
            ||  |    ||   |||||||| |  ||||||||||
Db     2824 TGCGCACCCCTCAAGCCTGCCAAGTCAGCT 2853


RESULT 12
5405942-15
;Patent No. 5405942
;      APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;      TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;      NUMBER OF SEQUENCES: 16
;      CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/07/65,673
;        FILING DATE: 16-JUN-1987
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: 630,557
;        FILING DATE: 19-JUL-1984
;SEQ ID NO:15:
;      LENGTH: 210
5405942-15

   Query Match            30.6%;  Score 165.2;  DB 6;  Length 210;
   Best Local Similarity  67.1%;  Pred. No. 1.5e-45;
   Matches  141;  Conservative  41;  Mismatches  28;  Indels   0;  Gaps   0;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||  ||||||  |:  :||||||||:||||:||:||| ||:|::|||::||:|:|:||| 
Db        1 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

```
            |||||||:::::|  ::|||||||||||||||  :|:|||:||||||  :|||||||||| || |||
Db     61  AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 120

Qy    121  ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || || |: |:|||:|||:|  :||::|||||||:|:||:|:  |||||||:|||||:|:|
Db    121  ACAGGUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180

Qy    181  TGTGTCCGCTGCAAGCCTACAAAGTCAGCT 210
            :| |  || |  || |||: | |||:||||:
Db    181  UGCGCACCCCUCAGGCCUGCCAAGUCAGCU 210


RESULT 13
US-08-308-196A-1
; Sequence 1, Application US/08308196A
; Patent No. 5612198
;  GENERAL INFORMATION:
;    APPLICANT:  Brierley, Russell A.
;    APPLICANT:  Davis, Geneva R.
;    APPLICANT:  Holtz, Gregory C.
;    APPLICANT:  Gleeson, Martin A.
;    APPLICANT:  Howard, Bradley D.
;    TITLE OF INVENTION:  Production of Insulin-Like Growth
;    TITLE OF INVENTION:  Factor-1 in Methylotrophic Yeast Cells
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/308,196A
;      FILING DATE:  09-SEPT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/983,523
;      FILING DATE:  03-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/578,728
;      FILING DATE:  04-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  51875
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 base pairs
;      TYPE:  nucleic acid
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  Query Match            29.9%;   Score 161.2;   DB 1;   Length 240;
  Best Local Similarity   84.6%;   Pred. No. 3.6e-44;
  Matches   181;  Conservative    0;  Mismatches  33;  Indels    0;  Gaps    0;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||| |||||| || ||||||||||||||| ||||| ||||| ||||||||||||||||
Db       17 GGACCGGAGACGCTCTGCGGGGCTGAGCTCGTGGATGCTCTGCAGTTCGTGTGTGGAGAC 76

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            |||||||||||| |||||||||||||||| |||||||||||| ||| |||| || |||
Db       77 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 136

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || ||||| ||||||||||| |||||||||||||||||||| |||||||| ||||||||
Db      137 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 196

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTT 214
            ||| | || ||||||| | |||||||||| | |
Db      197 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 230


RESULT 14
PCT-US91-06452-1
; Sequence 1, Application PC/TUS9106452
;   GENERAL INFORMATION:
;     APPLICANT:  Brierley, Russell A.
;     APPLICANT:  Davis, Geneva R.
;     APPLICANT:  Holtz, Gregory C.
;     APPLICANT:  Gleeson, Martin A.
;     APPLICANT:  Bradley, D. H.
;     TITLE OF INVENTION:  Production of Insulin-Like Growth
;     TITLE OF INVENTION:  Factor-1 in Methylotrophic Yeast Cells
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fitch, Even, Tabin & Flannery
;       STREET:  135 South LaSalle Street, Suite 900
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60603
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US91/06452
;       FILING DATE:  19910409
;       CLASSIFICATION:  435

  Query Match              29.9%;   Score 161.2;   DB 5;   Length 240;
  Best Local Similarity    84.6%;   Pred. No. 3.6e-44;
  Matches   181;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||| |||||| || ||||||||||||||| ||||| ||||| |||||||||||||||||
Db       17 GGACCGGAGACGCTCTGCGGGGCTGAGCTCGTGGATGCTCTGCAGTTCGTGTGTGGAGAC 76

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||| ||||||||||||||||| |||||||||||| ||| |||| || |||
Db       77 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 136

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || |||||| |||||||||| ||||||||||||||||||||| |||||||| ||||||||
Db      137 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 196

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTT 214
            || |   ||   |||||||| | ||||||||| | |
Db      197 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 230

   Query Match              29.9%;  Score 161.2;  DB 3;  Length 390;
   Best Local Similarity    84.6%;  Pred. No. 4.8e-44;
   Matches  181;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            ||||| ||||| || |||||||||||||| ||||| ||||| ||||||||||||||||||
Db      160 GGACCGGAGACGCTCTGCGGGGCTGAGCTCGTGGATGCTCTGCAGTTCGTGTGTGGAGAC 219

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||| ||||||||||||||| ||||||||||||||| ||| |||| || |||
Db      220 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 279

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || ||||| .|||||||||| |||||||||||||||||||| |||||||| ||||||||
Db      280 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 339

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTT 214
            || |  | |   ||||||| | |||||||| | |
Db      340 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 373


Search completed: December 13, 2003, 11:44:49
Job time : 49.8379 secs

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OM nucleic - nucleic search, using sw model

Run on:          December 13, 2003, 07:29:55 ; Search time 240.655 Seconds
                                            (without alignments)
                                            7443.919 Million cell updates/sec


Title:           US-09-852-261-3
Perfect score:   539
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters:      4403344

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 13:  /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
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                 18:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result          Query
   No.   Score  Match Length DB   ID                          Description

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      1      539   100.0     539    9   US-09-852-261-3        Sequence 3, Appli
      2    453.8    84.2     651   15   US-10-161-088-1        Sequence 1, Appli
      3      425    78.8     487    9   US-09-852-261-11       Sequence 11, Appl
      4    356.8    66.2     523    9   US-09-852-261-5        Sequence 5, Appli
      5    325.2    60.3     517    9   US-09-852-261-1        Sequence 1, Appli
      6    274.2    50.9    7260   10   US-09-919-497-24       Sequence 24, Appl
      7    274.2    50.9    7260   10   US-09-880-107-3739     Sequence 3739, Ap
      8    274.2    50.9    7260   13   US-09-873-319-707      Sequence 707, App
      9    274.2    50.9    7260   13   US-09-960-706-1066     Sequence 1066, Ap
     10    274.2    50.9    7260   15   US-10-136-639-4        Sequence 4, Appli
     11    272.6    50.6     725   15   US-10-207-655-54       Sequence 54, Appl
     12      262    48.6     471    9   US-09-852-261-13       Sequence 13, Appl
     13      224    41.6     612   13   US-10-251-661-7        Sequence 7, Appli
     14    213.8    39.7     286   15   US-10-161-088-3        Sequence 3, Appli
     15    206.8    38.4     318    9   US-09-852-261-9        Sequence 9, Appli
     16    203.6    37.8     462   15   US-10-238-114-1        Sequence 1, Appli
     17    168.4    31.2     210   13   US-09-807-742-18       Sequence 18, Appl
     18    166.8    30.9    2862   13   US-10-241-596-13       Sequence 13, Appl
     19    164.6    30.5    4532   10   US-09-930-377B-1       Sequence 1, Appli
     20    163.6    30.4     210   10   US-09-930-377B-2       Sequence 2, Appli
     21    161.2    29.9     390   15   US-10-179-046-13       Sequence 13, Appl
     22    143.6    26.6     182   13   US-10-029-386-18231    Sequence 18231, A
     23    143.6    26.6     516   13   US-10-029-386-5832     Sequence 5832, Ap
     24    124.2    23.0     213   15   US-10-076-816-9        Sequence 9, Appli
     25    124.2    23.0     213   15   US-10-077-381-9        Sequence 9, Appli
     26    118.6    22.0     621    9   US-09-921-398-40       Sequence 40, Appl
     27    118.6    22.0     621   15   US-10-280-826-40       Sequence 40, Appl
     28    105.4    19.6     480    9   US-09-921-398-38       Sequence 38, Appl
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     30     91.6    17.0     210   13   US-09-807-742-19       Sequence 19, Appl
     31     67.4    12.5     411   10   US-09-960-352-2082     Sequence 2082, Ap
c    32     67.2    12.5     437   15   US-10-066-543-663      Sequence 663, App
c    33     67.2    12.5     493   15   US-10-066-543-997      Sequence 997, App
c    34     67.2    12.5     518   15   US-10-066-543-1040     Sequence 1040, Ap
c    35     67.2    12.5     536   15   US-10-066-543-428      Sequence 428, App
     36     67.2    12.5     543   15   US-10-136-841-1        Sequence 1, Appli
c    37     67.2    12.5     549   15   US-10-066-543-478      Sequence 478, App
c    38     67.2    12.5     574    9   US-09-922-217-918      Sequence 918, App
c    39     67.2    12.5     574   10   US-09-833-263-918      Sequence 918, App
c    40     67.2    12.5     574   14   US-10-025-380-918      Sequence 918, App
c    41     67.2    12.5     577   15   US-10-066-543-1137     Sequence 1137, Ap
c    42     67.2    12.5     579   15   US-10-066-543-1094     Sequence 1094, Ap
c    43     67.2    12.5     586   15   US-10-066-543-808      Sequence 808, App
     44     67.2    12.5    1045   13   US-09-873-319-423      Sequence 423, App
     45     67.2(   12.5    1045   13   US-09-960-706-675      Sequence 675, App
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ALIGNMENTS


RESULT 1
US-09-852-261-3
; Sequence 3, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;   APPLICANT: GOLDSPINK, GEOFFREY

   Query Match              100.0%;  Score 539;  DB 9;  Length 539;
   Best Local Similarity    100.0%;  Pred. No. 8.4e-169;
   Matches  539;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
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Qy     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
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Qy    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
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Db    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
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Db    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539


RESULT 2

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  Query Match           84.2%;  Score 453.8;  DB 15;  Length 651;
  Best Local Similarity  92.8%;  Pred. No. 2.3e-140;
  Matches  476;  Conservative   0;  Mismatches  37;  Indels   0;  Gaps    0;


Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      139 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 198


Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
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Db      199 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 258


Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db      259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318


Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            |||| ||      ||||||||||   |||| || || ||||| ||||||||||||||||||
Db      319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 378


Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
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Db      379 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438


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Db      439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498


Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            |||||||||||||||||||||||| ||| |||||||||||| ||||||||| ||||||||
Db      499 CAGAATGTAGGAGGAGCCTCCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558


Qy      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
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Db      559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618

Qy      481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAA 513
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Db      619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651


RESULT 3
US-09-852-261-11
; Sequence 11, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDSPINK, GEOFFREY
;  APPLICANT:  TERENGHI, GIORGIO
;  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;  FILE REFERENCE: 117-351
;  CURRENT APPLICATION NUMBER: US/09/852,261
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: GB 0011278.9
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 487
;   TYPE: DNA
;   ORGANISM: Rattus sp.
US-09-852-261-11

  Query Match              78.8%;  Score 425;  DB 9;  Length 487;
  Best Local Similarity    90.4%;  Pred. No. 7.6e-131;
  Matches  487;  Conservative    0;  Mismatches    0;  Indels  52;  Gaps    1;

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Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
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Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
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Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
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Db      256 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 308

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Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
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Db     369 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 428

Qy     481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCCCGGAATTC 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 4
US-09-852-261-5
; Sequence 5, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDSPINK, GEOFFREY
;  APPLICANT:  TERENGHI, GIORGIO
;  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;  FILE REFERENCE: 117-351
;  CURRENT APPLICATION NUMBER: US/09/852,261
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: GB 0011278.9
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 523
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
US-09-852-261-5

  Query Match              66.2%;   Score 356.8;  DB 9;   Length 523;
  Best Local Similarity    82.3%;   Pred. No. 4.2e-108;
  Matches  436;  Conservative   0;  Mismatches   87;  Indels    7;  Gaps    2;

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Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           ||||| |||||| || |||||| ||||||||||||||| |||||||||||||||||||||
Db       1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           |||||||||||| ||||||||||||||| || |||||||||| |||||||||||| |||
Db      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           || |||||| |||||||||||| |||||||||||||||||||||||||||||||||||||
Db     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           |||| || |||||| ||||| |||| || ||| |||| ||||||||||||||| |||
Db     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
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Db    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
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Qy    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
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Db    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474

Qy    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
          |||||||| |||| |||||||||| ||||||||||||||||||||||||||||
Db    475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523


RESULT 5
US-09-852-261-1
; Sequence 1, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;   APPLICANT: GOLDSPINK, GEOFFREY
;   APPLICANT:  TERENGHI, GIORGIO
;   TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;   FILE REFERENCE: 117-351
;   CURRENT APPLICATION NUMBER: US/09/852,261
;   CURRENT FILING DATE:  2001-05-10
;   PRIOR APPLICATION NUMBER: GB 0011278.9
;   PRIOR FILING DATE: 2000-05-10
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 517
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-852-261-1

  Query Match             60.3%;   Score 325.2;  DB 9;   Length 517;
  Best Local Similarity   81.2%;   Pred. No. 1.4e-97;
  Matches  429;  Conservative    0;  Mismatches   88;  Indels  11;  Gaps    4;

Qy      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
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Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
          |||||||||| ||||||||||||||| |||||||||||||| |||||||||| || |||
Db     61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          || |||||| |||||||||| |||||||||||||||||||||||| |||||||||||||||||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
          ||| | || |||||||| | |||||||||| || |||| |||||||||||||||| |||
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Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
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Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
           |||||||||||||||||| ||||||||||||||||||||| ||||||||||||||| |||
Db     298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||| ||||| || || ||| | |||||    | || | || | |||||||| || ||||||
Db     358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy     421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
           ||          |       |||||| |||| ||| ||||       || ||| |||| ||
Db     417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAATAAGTTTGATC 470

Qy     481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACAT 528
           ||||||| |||| ||||||||||| ||||||||||||||||||||||||
Db     471 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACAT 517


RESULT 6
US-09-919-497-24
; Sequence 24, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
;  APPLICANT: Mutter, George L.
;  TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
;  FILE REFERENCE: B0801/7225
;  CURRENT APPLICATION NUMBER: US/09/919,497
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/221,735
;  PRIOR FILING DATE: 2000-07-31
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
;    LENGTH: 7260
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-919-497-24

  Query Match              50.9%;  Score 274.2;  DB 10;  Length 7260;
  Best Local Similarity    76.0%;  Pred. No. 5.7e-80;
  Matches  405;  Conservative    0;  Mismatches   68;  Indels   60;  Gaps   3;

Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           |||||| |||||| || ||||||||||||||||||||||| |||||||||||||||||||
Db     311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           |||||||||||| |||||||||||||||| ||||||||||||||| ||||||||| || |||
Db     371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           || |||| |||||||||||||| |||||||||||||||||| |||||||||||||||||||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
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Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
          ||  |   |  |   |||||||| | |||||||||||| ||  |||| |||||||||||||||| |||
Db    491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
          ||||||||||||| |||
Db    551 ATGCCCAAGACCCAG--------------------------------------------- 565

Qy    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                 |||||||||||| ||||||||| ||||||||| |||||||||||||||||| |||
Db    566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
          ||| ||||||||| || ||||| |||||     |  | || || | |||||||| ||||||||||
Db    619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy    421 --CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAA 478
            ||||   |||   |||||   |||| | |||||||||| |||        || ||| ||||   |
Db    679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCA------AAAAATAAGTTTGA 732

Qy    479 TATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
          ||  |||||| | ||||||||| |||||| ||||||||||||||||||||||||||||
Db    733 TAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTCC 785


RESULT 7
US-09-880-107-3739
; Sequence 3739, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3739
;  LENGTH: 7260
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025
US-09-880-107-3739

  Query Match        50.9%;  Score 274.2;  DB 10;  Length 7260;
  Best Local Similarity   76.0%;  Pred. No. 5.7e-80;
  Matches  405;  Conservative   0;  Mismatches  68;  Indels  60;  Gaps   3;
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Qy      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
          |||||  |||||| || |||||||||||||||||||||||| |||||||||||||||||||
Db    311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
          ||||||||||| |||||||||||||||||  ||||||||||||| |||||||| || |||
Db    371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          || |||||| ||||||||||| |||||||||||||||||||||||||| |||||||||||||
Db    431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
          || |   | |   ||||||| | ||||||||||| ||   |||| ||||||||||||| |||
Db    491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
          ||||||||||| |||
Db    551 ATGCCCAAGACCCAG--------------------------------------------- 565

Qy    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                |||||||||| |||||||| |||||||||| |||||||||||||||||| |||
Db    566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
          ||| |||||||| || |||||  |||||      | | || || | |||||||| ||||||||
Db    619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy    421 --CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAA 478
            ||||   |||  |||||  |||| | |||||||||| |||      || ||| |||| |
Db    679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCA------AAAAATAAGTTTGA 732

Qy    479 TATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
          || |||||| | ||||||||| ||||||| |||||||||||||||||||||||||
Db    733 TAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTCC 785
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RESULT 8
US-09-873-319-707
; Sequence 707, Application US/09873319A
; Publication No. US20030134324A1
; GENERAL INFORMATION:
;  APPLICANT: Munger, William E.
;  APPLICANT: Kulkarni, Prakash
;  APPLICANT: Getzenberg, Robert H.
;  APPLICANT: Waga, Iwao
;  APPLICANT: Yamamoto, Jun
;  TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
;  TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
;  FILE REFERENCE: 44921-5029-US
;  CURRENT APPLICATION NUMBER: US/09/873,319A
;  CURRENT FILING DATE: 2001-06-05
;  EARLIER APPLICATION NUMBER: US 60/223,323
;  EARLIER FILING DATE: 2000-08-07
;  NUMBER OF SEQ ID NOS: 755
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 707

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  Query Match              50.9%;  Score 274.2;  DB 13;  Length 7260;
  Best Local Similarity    76.0%;  Pred. No. 5.7e-80;
  Matches  405;  Conservative    0;  Mismatches   68;  Indels   60;  Gaps     3;

Qy         1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
             |||||  ||||||  ||  |||||||||||||||||||||||  ||||||||||||||||||||
Db       311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy        61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
             |||||||||||| ||||||||||||||||||  |||||||||||| ||||||||| || |||
Db       371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy       121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
             || |||||  ||||||||||| |||||||||||||||||||| |||||||||||||||||||
Db       431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy       181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
             || |   | |   |||||||| | |||||||||||| ||   |||| ||||||||||| |||
Db       491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy       241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
             ||||||||||| |||
Db       551 ATGCCCAAGACCCAG--------------------------------------------- 565

Qy       301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                    |||||||||| ||||||||| |||||||||| |||||||||||||||||||| |||
Db       566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy       361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
             ||| ||||||||| || ||||| |||||     | | || || | |||||||| |||||||||
Db       619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy       421 --CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAA 478
               ||||   |||  ||||| |||| | |||||||||| |||         || ||| ||||  |
Db       679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCA------AAAAATAAGTTTGA 732

Qy       479 TATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
             || ||||| | |||||||| |||||| ||||||||||||||||||||||||||||
Db       733 TAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTCC 785
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RESULT 9
US-09-960-706-1066
; Sequence 1066, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
;   APPLICANT: Munger, William E.
;   TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
Hyperplasia Using
;   TITLE OF INVENTION:  Gene Expression Profiles

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  Query Match             50.9%;  Score 274.2;  DB 13;  Length 7260;
  Best Local Similarity   76.0%;  Pred. No. 5.7e-80;
  Matches  405;  Conservative    0;  Mismatches   68;  Indels   60;  Gaps    3;

Qy       1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
           |||||  ||||||  ||  ||||||||||||||||||||||| |||||||||||||||||||
Db     311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
           ||||||||||| ||||||||||||||||||||   |||||||||||| |||||||| || |||
Db     371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           || ||||| ||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           || |  | |  ||||||| | ||||||||||| || |||| ||||||||||||||| |||
Db     491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           |||||||||||| |||
Db     551 ATGCCCAAGACCCAG--------------------------------------------- 565

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                  ||||||||||| ||||||||| |||||||||| ||||||||||||||||| |||
Db     566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
           ||| |||||||| || ||||| ||||    | | || || | |||||||| ||||||||
Db     619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 --CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAA 478
             ||||   |||  ||||| ||||| | |||||||||| |||        || ||| |||| |
Db     679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCA------AAAAATAAGTTTGA 732

Qy     479 TATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
           || ||||| | ||||||||| |||||| ||||||||||||||||||||||||||
Db     733 TAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTCC 785
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RESULT 10
US-10-136-639-4
; Sequence 4, Application US/10136639
; Publication No. US20030072761A1
; GENERAL INFORMATION:
;   APPLICANT: LeBowitz, Jonathan
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS
THE BLOOD BRAIN
;   TITLE OF INVENTION:  BARRIER
;   FILE REFERENCE: SYM-008
;   CURRENT APPLICATION NUMBER: US/10/136,639
;   CURRENT FILING DATE:  2002-09-06
;   PRIOR APPLICATION NUMBER: US 60/329,650
;   PRIOR FILING DATE: 2001-10-16
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 7260
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-136-639-4

  Query Match            50.9%;  Score 274.2;  DB 15;  Length 7260;
  Best Local Similarity  76.0%;  Pred. No. 5.7e-80;
  Matches  405;  Conservative  0;  Mismatches  68;  Indels  60;  Gaps  3;

Qy         1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
             |||||  |||||| || |||||||||||||||||||||| |||||||||||||||||||||
Db       311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy        61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
             ||||||||||| |||||||||||||||| ||||||||||||| |||||||| || |||
Db       371 AGGGGCTTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy       121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
             || |||||| ||||||||||||| |||||||||||||||||||| |||||||||||||||||
Db       431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy       181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
             || |  || |||||| | ||||||||||| || |||| |||||||||||||| |||
Db       491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy       241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
             ||||||||||| |||
Db       551 ATGCCCAAGACCCAG--------------------------------------------- 565

Qy       301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                    |||||||||| ||||||||| ||||||||||| |||||||||||||||||| |||
Db       566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy       361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
             ||| ||||||||| || ||||| |||||     | | || || | |||||||| |||||||||
Db       619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy       421 --CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAA 478
               ||||  ||| |||||  |||| | |||||||||| |||      || ||| |||| |

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Db      679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCA------AAAAATAAGTTTGA 732

Qy      479 TATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
            || ||||||  | ||||||||| ||||||  |||||||||||||||||||||||||||||
Db      733 TAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTCC 785


RESULT 11
US-10-207-655-54
; Sequence 54, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
;   LENGTH: 725
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-207-655-54

   Query Match           50.6%;  Score 272.6;  DB 15;  Length 725;
   Best Local Similarity  75.8%;  Pred. No. 5.6e-80;
   Matches  404;  Conservative    0;  Mismatches  69;  Indels  60;  Gaps    3;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||  |||||  ||  ||||||||||||||||||||||||| ||||||||||||||||||
Db      156 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 215

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            ||||||||||| |||||||||||||||||  ||||||||||||| |||||||||| || |||
Db      216 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 275

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            ||  || ||  ||||||||| ||||||||||||||||||||| |||||||||||||||||·
Db      276 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 335

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            ||| |  | |  |||||||| | |||||||||| ||   |||| |||||||||||||| |||
Db      336 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 395

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            |||||||||||| |||
Db      396 ATGCCCAAGACCCAG--------------------------------------------- 410

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                 .  |||||||||||| |||||||||| |||||||||| ||||||||||||||||| |||
Db      411 ------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 463

Qy      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
            ||| ||||||||| || ||||| |||||     | | || || | |||||||| ||||||||
Db      464 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 523
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Qy      421 --CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAA 478
            |||| ||| ||||| |||| | |||||||||| |||      || ||| ||||| |
Db      524 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCA------AAAAATAAGTTTGA 577

Qy      479 TATCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTCC 531
            || |||||| | |||||||||| |||||| ||||||||||||||||||||||||||||
Db      578 TAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTCC 630


RESULT 12
US-09-852-261-13
; Sequence 13, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDSPINK, GEOFFREY
;  APPLICANT:  TERENGHI, GIORGIO
;  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;  FILE REFERENCE: 117-351
;  CURRENT APPLICATION NUMBER: US/09/852,261
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: GB 0011278.9
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 471
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
US-09-852-261-13

  Query Match          48.6%;  Score 262;  DB 9;  Length 471;
  Best Local Similarity 74.7%;  Pred. No. 1.5e-76;
  Matches  396;  Conservative   0;  Mismatches   75;  Indels   59;  Gaps    3;

Qy        1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
            |||||| |||||| || ||||| ||||||||||||||| |||||||||||||||||||||
Db        1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy       61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
            |||||||||||| ||||||||||||||| || |||||||||| ||||||||||||| |||
Db       61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy      121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            || |||| |||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
            |||| | | |||||| ||||| |||| || ||| |||| |||||||||||| |||
Db      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
            |||||||||||||||
Db      241 ATGCCCAAGACTCAG-------------------------------------------- 255

Qy      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
            |||||||||||| ||||||||||||||||||||||| |||||||||||||||||| |||
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Db      256  -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy      361  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
             |||  |||||||| ||  ||| | |||||     | ||| | || | ||||||| || ||||||
Db      309  CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy      421  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
             ||          |       |||||| |||| ||| ||||         || ||| |||| ||
Db      369  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 422

Qy      481  TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
             |||||||| |||| |||||||||||| ||||||||||||||||||||||||||
Db      423  ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471
```

RESULT 13
US-10-251-661-7
; Sequence 7, Application US/10251661
; Publication No. US20030166555A1
; GENERAL INFORMATION:
;   APPLICANT: Alberini, Cristina M.
;   APPLICANT:  Bear, Mark F.
;   TITLE OF INVENTION: Methods and Compositions for Regulating
;   TITLE OF INVENTION:  Memory Consolidation
;   FILE REFERENCE: 3499.1001-003
;   CURRENT APPLICATION NUMBER: US/10/251,661
;   CURRENT FILING DATE:  2002-09-20
;   PRIOR APPLICATION NUMBER: 60/193,614
;   PRIOR FILING DATE: 2000-03-31
;   PRIOR APPLICATION NUMBER: PCT/US01/10661
;   PRIOR FILING DATE: 2001-04-02
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 612
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (151)...(564)
US-10-251-661-7

  Query Match              41.6%;   Score 224;   DB 13;   Length 612;
  Best Local Similarity    75.6%;   Pred. No. 8e-64;
  Matches  316;  Conservative     0;  Mismatches    50;  Indels   52;  Gaps      1;

```
Qy        1  GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
             |||||  ||||| || |||||||||||||||||||||||||| ||||||||||||||||||||
Db      247  GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 306

Qy       61  AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
             |||||||||||| |||||||||||||||| |||||||||||||| ||||||||| || |||
Db      307  AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 366

Qy      121  ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
             || ||||| |||||||||||| ||||||||||||||||||||| ||||||||||||||||||
Db      367  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 426
```

```
Qy     181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
           || |   | |   |||||||| | |||||||||||| ||  |||| |||||||||||||||| |||
Db     427 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 486

Qy     241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
           |||||||||||| |||
Db     487 ATGCCCAAGACCCAG--------------------------------------------- 501

Qy     301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
                  |||||||||| ||||||||| |||||||||| ||||||||||||||||||| |||
Db     502 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 554

Qy     361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTT 418
           ||| ||||||||| || ||||| |||||    |  | || || | |||||||| |||||||
Db     555 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTT 612
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RESULT 14
US-10-161-088-3
; Sequence 3, Application US/10161088
; Publication No. US20030077761A1
; GENERAL INFORMATION:
; APPLICANT: Parrow, Vendela
; APPLICANT:  Rosengren, Linda
; TITLE OF INVENTION: NEW METHODS
; FILE REFERENCE: 13425-111001
; CURRENT APPLICATION NUMBER: US/10/161,088
; CURRENT FILING DATE:  2002-05-31          •
; PRIOR APPLICATION NUMBER: SE 0101934-8
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 286
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-161-088-3

  Query Match              39.7%;  Score 213.8;  DB 15;  Length 286;
  Best Local Similarity    89.5%;  Pred. No. 1.3e-60;
  Matches  230;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

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Qy      16 TGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCAAGGGGCTTTTACTTC 75
           |||||||||||||||||||||||| |||||||||||||||||||||||| |||||||||||||
Db      18 TGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCGAGGGGCTTTTACTTC 77

Qy      76 AACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAGACGGGCATTGTGGAT 135
           |||||||||||| ||||||||||||||||||||||||||||| ||||| |||||||||||||
Db      78 AACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAGACAGGCATTGTGGAT 137

Qy     136 GAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGTCCGCTGCAAG 195
           ||||||||||||||||||||||||||||||||||| ||||||||||||||| ||     |||
Db     138 GAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTACTGTGCCCCACTGAAG 197

Qy     196 CCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACATGCCCAAGACTCAG 255
           ||||||||   |||| || || ||||| |||||||||||||||||||||||||||||||||||
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Db        198 CCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGACATGCCCAAGACTCAG 257
                                     (
Qy        256 AAGTCCCAGCCCCTATC 272
                  | | ||| | ||
Db        258 GCATGCAAGCTTGTCTC 274
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```
RESULT 15
US-09-852-261-9
; Sequence 9, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDSPINK, GEOFFREY
;  APPLICANT:  TERENGHI, GIORGIO
;  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;  FILE REFERENCE: 117-351
;  CURRENT APPLICATION NUMBER: US/09/852,261
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: GB 0011278.9
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;    LENGTH: 318
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-852-261-9
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   Query Match           38.4%;  Score 206.8;  DB 9;  Length 318;
   Best Local Similarity  87.6%;  Pred. No. 3e-58;
   Matches  226;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
          ||||| |||||| || |||||||||||||||||||| |||||||||||||||||||||||
Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
          |||||||||||| |||||||||||||||| ||||||||||||| ||||||||| || |||
Db     61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          || ||||| ||||||||||| |||||||||||||||||||| ||||||||||||||||||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
          || | | | ||||||| | ||||||||||| || |||| |||||||||||||| |||
Db    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAG 258
          |||||||||| ||||||
Db    241 ATGCCCAAGACCCAGAAG 258
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Search completed: December 13, 2003, 11:56:46
Job time : 241.655 secs
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